```
                Copyright    GenCore version 5.1.6
                             (c) 1993 - 2003  Compugen Ltd.

.OM protein - protein search, using sw model

Run on:         November 25, 2003, 16:39:44  ;Search time 17 Seconds
                                              (without alignments)
                             597.516 Million cell updates/sec

Title:          US-09-666-267B-8
Perfect score:  1149
Sequence:       1 GLSHFCSGVIHVTKEVKEVA..........LRVNQTFNWNTTKQEHFPDN 216

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:          127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SwissProt_41:*

                          SUMMARIES

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1149	100.0	288	1	CD80_HUMAN	P33681 homo sapien
2	738	64.2	299	1	CD80_RABIT	P42070 oryctolagus
3	561	48.8	306	1	CD80_MOUSE	Q00609 mus musculu
4	182	15.8	329	1	CD86_HUMAN	P42081 homo sapien
5	161	14.0	302	1	ICOL_HUMAN	O75144 homo sapien
6	152	13.2	309	1	CD86_MOUSE	P42082 mus musculu
7	150.5	13.1	322	1	ICOL_MOUSE	Q9jh8 mus musculu
8	140.5	12.2	330	1	CD86_RABIT	P42071 oryctolagus
9	138	12.0	509	1	SHS1_RAT	P97710 r protein-t
10	134.5	11.7	583	1	C166_MOUSE	Q61490 mus musculu
11	133.5	11.6	583	1	C166_HUMAN	Q13740 homo sapien
12	129	11.2	221	1	BRF1_EBV	P03228 epstein-bar
13	127	11.1	526	1	BUTY_HUMAN	Q13410 homo sapien
14	122.5	10.7	588	1	C166_CHICK	P42292 gallus gall
15	120.5	10.5	513	1	SHS1_MOUSE	P97797 m protein-t
16	120	10.4	506	1	SHS1_BOVIN	O46631 bos taurus
17	119	10.4	524	1	BUTY_MOUSE	Q62556 mus musculu
18	116.5	10.1	1088	1	NCA1_XENLA	P16170 xenopus lae
19	115	10.0	761	1	NCA2_HUMAN	P13592 homo sapien
20	115	10.0	848	1	NCA1_HUMAN	P13591 homo sapien
21	110.5	9.6	321	1	TCB_FLV	P11364 feline leuk
22	110	9.6	398	1	SRB1_HUMAN	O00241 homo sapien
23	109.5	9.5	646	1	MU18_HUMAN	Q43121 homo sapien
24	109.5	9.5	853	1	NCA1_BOVIN	P31836 bos taurus
25	109	9.5	387	1	SRB2_HUMAN	Q9p1w8 homo sapien
26	109	9.5	526	1	BUTY_BOVIN	P18892 bos taurus
27	109	9.5	2029	1	LAR_DROME	P16621 drosophila
28	108.5	9.4	365	1	CXAR_MOUSE	P97792 mus musculu
29	107.5	9.4	333	1	AMAL_DROME	P15364 drosophila
30	106.5	9.3	858	1	NCA1_RAT	P13596 rattus norv
31	105	9.1	319	1	A33_HUMAN	Q99795 homo sapien
32	105	9.1	1091	1	NCA1_CHICK	P13590 gallus gall
33	104	9.1	1092	1	NCA2_XENLA	P36335 xenopus lae
34	103.5	9.0	725	1	NCA2_MOUSE	P13594 mus musculu
35	103.5	9.0	1115	1	NCA1_MOUSE	P13595 mus musculu
36	103	9.0	298	1	JAM2_HUMAN	P57087 homo sapien
37	102.5	8.9	503	1	SHS1_HUMAN	P78324 h protein-t
38	102	8.9	1443	1	NEO1_CHICK	Q90610 gallus gall
39	101.5	8.8	403	1	RAGE_MOUSE	Q62151 mus musculu
40	100	8.7	413	1	HEMO_MANSE	P31398 manduca sex
41	99.5	8.7	1338	1	VGR1_HUMAN	P17948 h vascular
42	98.5	8.6	365	1	CXAR_HUMAN	P78310 homo sapien
43	98.5	8.6	1242	1	NPHN_MOUSE	Q9qz87 mus musculu
44	98	8.5	278	1	OX2G_RAT	P04218 rattus norv
45	98	8.5	298	1	JAM1_BOVIN	Q9xt56 bos taurus

ALIGNMENTS

```
RESULT 1
CD80_HUMAN
ID   CD80_HUMAN     STANDARD;     PRT;     288 AA.
AC   P33681;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE   antigen) (CTLA-4 counter-receptor B7.1) (B7) (BB1).
GN   CD80 OR CD28LG1 OR CD28LG OR LAB7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoid;
RX   MEDLINE=90010147; PubMed=2794510;
RA   Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F.,
RA   Nadler L.M.;
RT   "B7, a new member of the Ig superfamily with unique expression on
RT   activated and neoplastic B cells.";
RL   J. Immunol. 143:2714-2722(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92307753; PubMed=1377173;
RA   Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C.,
RA   Dupont B.;
RT   "Genomic organization and chromosomal location of the human gene
RT   encoding the B-lymphocyte activation antigen B7.";
RL   Immunogenetics 36:175-181(1992).
RN   [3]
RP   SEQUENCE OF 35-38.
RX   MEDLINE=91341422; PubMed=1714935;
RA   Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J.,
RA   White M., Fingeroth J.D., Gribben J.G., Nadler L.M.;
RT   "Structure, expression, and T cell costimulatory activity of the
RT   murine homologue of the human B lymphocyte activation antigen B7.";
RL   J. Exp. Med. 174:625-631(1991).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=95088403; PubMed=7527824;
RA   Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
RA   Okumura K., Ito D., Azuma M.;
RT   "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
RT   cell proliferation, cytokine production, and generation of CTL.";
RL   J. Immunol. 154:97-105(1995).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.
RX   MEDLINE=20125021; PubMed=10661405;
RA   Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K.,
RA   Jones E.Y., Stuart D.I., Davis S.J.;
RT   "Structure and dimerization of a soluble form of B7-1.";
RL   Immunity 12:51-60(2000).
CC   -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC       LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
```

```
FT   TURN        155    156
FT   STRAND      157    167
FT   STRAND      171    177
FT   STRAND      181    182
FT   STRAND      186    191
FT   TURN        193    195
FT   STRAND      198    207
FT   TURN        208    209
FT   STRAND      212    220
FT   TURN        221    222
FT   STRAND      225    231
SQ   SEQUENCE   288 AA;  33048 MW;  BA453EE34528B1F4 CRC64;

     Query Match    100.0%;  Score 1149;  DB 1;  Length 288;
     Best Local Similarity  100.0%;
     Matches  216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;    Pred. No. 1.7e-88;

Qy      1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     27  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  86

Qy     61  YKQRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87  YKQRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy    121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy    181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
           ||||||||||||||||||||||||||||||||||||
Db    207  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242


RESULT 2
CD80_RABIT
ID   CD80_RABIT   STANDARD;     PRT;     299 AA.
AC   P42070;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE   antigen).
GN   CD80.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B/J X CHBB.HM;
RX   MEDLINE=95369849; PubMed=7642234;
RA   Isono T., Seto A.;
RT   "Cloning and sequencing of the rabbit gene encoding T-cell
RT   costimulatory molecules.";
RL   Immunogenetics 42:217-220(1995).
CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC     LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC     PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC     RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   ----------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------
DR   EMBL; D49843; BAA08643.1; -.
```

```
CC     PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC     RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
CC     AND DENDRITIC CELLS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD80 entry;
CC     WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd80.htm".
CC   ----------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------
DR   EMBL; M27533; AAA36045.1; -.
DR   EMBL; M83077; AAA58390.1; -.
DR   EMBL; M83072; AAA58390.1; JOINED.
DR   EMBL; M83073; AAA58390.1; JOINED.
DR   EMBL; M83074; AAA58390.1; JOINED.
DR   PIR; I54495; A45803.
DR   PDB; 1DR9; 10-JAN-01.
DR   PDB; 1I8L; 04-APR-01.
DR   Genew; HGNC:1700; CD80.
DR   MIM; 112203; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor; 3D-structure.
FT   SIGNAL         1     34
FT   CHAIN         35    288       T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT   DOMAIN        35    242       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     243    263       POTENTIAL.
FT   DOMAIN       264    288       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       135    230       IG-LIKE V-TYPE.
FT   DOMAIN       145    230       IG-LIKE C2-TYPE.
FT   DISULFID      50    116
FT   DISULFID     162    216
FT   CARBOHYD      53     53       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      89     89       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD      98     98       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     186    186       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     207    207       N-LINKED (GLCNAC...).
FT   CARBOHYD     211    211       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     226    226       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     232    232       N-LINKED (GLCNAC...) (POTENTIAL).
FT   STRAND        37     41
FT   STRAND        42     43
FT   STRAND        46     48
FT   TURN          56     57
FT   HELIX         58     61
FT   STRAND        63     68
FT   TURN          69     70
FT   STRAND        71     77
FT   TURN          78     79
FT   STRAND        80     83
FT   HELIX         85     88
FT   TURN          89     90
FT   STRAND        91     94
FT   TURN          96     99
FT   STRAND       100    103
FT   HELIX        108    110
FT   STRAND       112    120
FT   TURN         123    124
FT   TURN         127    139
FT   STRAND       146    151
```

```
DR   PIR; I46690; I46690.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor.
FT   SIGNAL        1     32       POTENTIAL.
FT   CHAIN        33    299       T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT   DOMAIN       33    243       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    244    264       POTENTIAL.
FT   DOMAIN      265    299       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       33    131       IG-LIKE V-TYPE.
FT   DOMAIN      144    225       IG-LIKE C2-TYPE.
FT   DISULFID     49    115       POTENTIAL.
FT   DISULFID    161    215       POTENTIAL.
FT   CARBOHYD     52     52       N-LINKED (GLCNAC. . .)   (POTENTIAL).
FT   CARBOHYD     88     88       N-LINKED (GLCNAC. . .)   (POTENTIAL).
FT   CARBOHYD     97     97       N-LINKED (GLCNAC. . .)   (POTENTIAL).
FT   CARBOHYD    122    122       N-LINKED (GLCNAC. . .)   (POTENTIAL).
FT   CARBOHYD    185    185       N-LINKED (GLCNAC. . .)   (POTENTIAL).
FT   CARBOHYD    206    206       N-LINKED (GLCNAC. . .)   (POTENTIAL).
FT   CARBOHYD    210    210       N-LINKED (GLCNAC. . .)   (POTENTIAL).
SQ   SEQUENCE    299 AA;   33513 MW;  6744223S5CC91DE0 CRC64;

Query Match             64.2%;  Score 738;  DB 1;  Length 299;
Best Local Similarity   63.9%;  Pred. No. 2.6e-54;
Matches  133;  Conservative  36;  Mismatches  39;  Indels  0;  Gaps  0;

Qy         4 HFCSGVIHVTKEVEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKN 63
             || ||| ||||: :|::||||| || :|:||||||||| ||:|||| :::|||||||||
Db        29 HFSSGISQVTKSVKEMAALSCDYNISIDELARMRIYWQKDQQMVLSIISGQVEVWPEYKN 88

Qy        64 RTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISD 123
             || |  | |||| |||| |:|: |||||| :|| |: |:|| ||| |:: |||||| :|:
Db        89 RTFPDIINNLSLMILALRLSDKGTYTCVVQKNENGSFRRREHLTSVTLSIRADFPVPSITD 148

Qy       124 FEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMT 183
             |||||||||||| :| ||||||||||||::|:|||| ||| |||||||| ||| ||||| |
Db       149 IGHPDNVKRIRCSASGGFPEPRLAWMEDGEELNAVNTTVDQDLDTELYSVSSELDFNVT 208

Qy       184 TNHSFMCLIKYGHLRVNQTFNWNTTKQE 211
             |:|| ||||||||:| :| |||||:|:|
Db       209 NNHSIVCLIKYGELSVSQIFPWSKPKQE 236
```

RESULT 3

```
CD80_MOUSE
ID   CD80_MOUSE    STANDARD;    PRT;    306 AA.
AC   Q00609;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE   antigen) (B7).
GN   CD80 OR B7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RX   MEDLINE=91341422; PubMed=1714935;
RA   Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J.,
RA   White M., Fingeroth J.D., Gribben J.G., Nadler L.M.;
RT   "Structure, expression, and T cell costimulatory activity of the
RT   murine homologue of the human B lymphocyte activation antigen B7.";
RL   J. Exp. Med. 174:625-631(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RX   MEDLINE=93077789; PubMed=7686531;
RA   Selvakumar A., White P.C., Dupont B.;
RT   "Genomic organization of the mouse B-lymphocyte activation antigen
RT   B7.";
RL   Immunogenetics 38:292-295(1993).
CC   -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC       LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC       PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC       RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA
CC       INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL
CC       MALIGNANCIES.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-
CC       ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND
CC       IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like v-type domain.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; X60958; CAA43291.1; -.
DR   EMBL; L12589; AAA37240.1; ALT_SEQ.
DR   EMBL; L12585; AAA37240.1; JOINED.
DR   EMBL; L12586; AAA37240.1; JOINED.
DR   EMBL; L12587; AAA37240.1; JOINED.
DR   EMBL; L12588; AAA37240.1; JOINED.
DR   PIR; I49503; I49503.
DR   HSSP; P33681; 1DR9.
DR   MGD; MGI:101775; Cd80.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor.
FT   SIGNAL        1     37       
FT   CHAIN        38    306       T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT   DOMAIN       38    246       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    247    268       POTENTIAL.
FT   DOMAIN      269    306       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       38    135       IG-LIKE V-TYPE.
FT   DOMAIN      148    229       IG-LIKE C2-TYPE.
FT   DOMAIN      227    246       IG-HINGE LIKE (POTENTIAL).
FT   DISULFID     54    119       .
FT   DISULFID    165    219       POTENTIAL.
FT   CARBOHYD     93     93       N-LINKED (GLCNAC. . .)   (POTENTIAL).
FT   CARBOHYD     99     99       N-LINKED (GLCNAC. . .)   (POTENTIAL).
FT   CARBOHYD    149    149       N-LINKED (GLCNAC. . .)   (POTENTIAL).
FT   CARBOHYD    189    189       N-LINKED (GLCNAC. . .)   (POTENTIAL).
FT   CARBOHYD    210    210       N-LINKED (GLCNAC. . .)   (POTENTIAL).
FT   CARBOHYD    214    214       N-LINKED (GLCNAC. . .)   (POTENTIAL).
SQ   SEQUENCE    306 AA;   34589 MW;  1DBADE0931B84C62 CRC64;

Query Match             48.8%;  Score 561;  DB 1;  Length 306;
Best Local Similarity   50.7%;  Pred. No. 1.4e-39;
Matches  104;  Conservative  41;  Mismatches  58;  Indels  2;  Gaps  2;

Qy        12 VTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITN 71
             ::||||: ||::||||:|::|||||  |||||||| |||:|||| :::|||||||||| |
Db        42 LSKSVKDKVLLPCRYNSPHEDESEDRIYWQKHDKVVLSVIAGKLKVWPEYKNRTLYDNT- 100

Qy        72 NLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNI 131
```

```
Db      101  TYSLIILGLVLSDRGTYSCVVQKKERGTYEVKHLALVKLSIKADFSTPNITESGNPSADT 160
             |::||   ||||  |||| || ||| |||||||||| ||:||:   |:|:||||||  |:::
Qy      132  RRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTNHSFMCL  191
             :||:|  ||||||| |||||| |||||||||||||:||||||:|:|||| |||:||||:||
Db      161  KRITCFASGGFPKPRRFSWLENGRELPGINTTISQDPESELYTISSQLDFNTTRNHTIKCL 220

Qy      192  IKYGHLRVNQTFNWNTKQEHFPDN 216
             ||||  :|:   |:: |:||
Db      221  IKYGDAHVSEDFTWEKPPEDP-PDS 244


RESULT 4
CD86_HUMAN
ID   CD86_HUMAN    STANDARD;    PRT;     329 AA.
AC   P42081; Q13655;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE   antigen) (CTLA-4 counter-receptor B7.2) (B70) (FUN-1) (BU63).
GN   CD86 OR CD28LG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94053735; PubMed=7694363;
RA   Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,
RA   Restivo V.A. Jr., Lombard L.A., Gray G.S., Nadler L.M.;
RT   "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
RT   cell proliferation.";
RL   Science 262:909-911(1993).
RN   [2]
RP   SEQUENCE OF 7-329 FROM N.A.
RX   MEDLINE=94050123; PubMed=7694153;
RA   Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,
RA   Lanier L.L., Somoza C.;
RT   "B70 antigen is a second ligand for CTLA-4 and CD28.";
RL   Nature 366:76-79(1993).
RN   [3]
RP   SEQUENCE OF 7-329 FROM N.A.
RC   TISSUE=Foreskin;
RX   MEDLINE=95311831; PubMed=7541777;
RA   Jellis C.L., Wang S.S., Rennert P., Borriello F., Sharpe A.H.,
RA   Green N.R., Gray G.S.;
RT   "Genomic organization of the gene coding for the costimulatory human
RT   B-lymphocyte antigen B7-2 (CD86).";
RL   Immunogenetics 42:85-89(1995).
RN   [4]
RP   SEQUENCE OF 7-329 FROM N.A.
RX   MEDLINE=95088403; PubMed=7527824;
RA   Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
RA   Okumura K., Ito D., Azuma M.;
RT   "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
RT   cell proliferation, cytokine production, and generation of CTL.";
RL   J. Immunol. 154:97-105(1995).
RN   [5]
RP   IDENTIFICATION AS CD86.
RX   MEDLINE=94348060; PubMed=7520767;
RA   Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,
RA   Nadler L.M., Wakasa H., Tedder T.F.;
RT   "The B7-2 (B70) costimulatory molecule expressed by monocytes and
RT   activated B lymphocytes is the CD86 differentiation antigen.";
RL   Blood 84:1402-1407(1994).
CC   -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC       FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC       BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC       EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC       SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CC       CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND
CC       MONOCYTES.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD86 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd86.htm".
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; L25259; AAA58389.1; -.
DR   EMBL; U04343; AAB03814.1; -.
DR   EMBL; U17722; AAA86473.1; -.
DR   EMBL; U17717; AAA86473.1; JOINED.
DR   EMBL; U17718; AAA86473.1; JOINED.
DR   EMBL; U17719; AAA86473.1; JOINED.
DR   EMBL; U17721; AAA86473.1; JOINED.
DR   PIR; A48754; A48754.
DR   PDB; 1I85; 04-APR-01.
DR   Genew; HGNC:1705; CD86.
DR   MIM; 601020; -.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0006955; P:immune response; TAS.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor; Polymorphism; 3D-structure.
FT   SIGNAL        1     23
FT   CHAIN        24    329       T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT   DOMAIN       24    247       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    248    268       POTENTIAL.
FT   DOMAIN      269    329       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       33    131       IG-LIKE V-TYPE.
FT   DOMAIN      150    225       IG-LIKE C2-TYPE.
FT   DISULFID     40    110       POTENTIAL.
FT   DISULFID    157    218       POTENTIAL.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD     47     47       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    146    146       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    154    154       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    177    177       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    192    192       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    213    213       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   VARIANT     310    310       A -> T (in dbSNP:1129055).
FT                                /FTId=VAR_014650.
FT   CONFLICT     27     27       K -> E (IN REF. 3).
SQ   SEQUENCE   329 AA;  37696 MW;  65D4F3826889CF7D CRC64;

Query Match             15.8%;  Score 182;  DB 1;  Length 329;
Best Local Similarity   29.0%;  Pred. No. 4.9e-08;
Matches    60;  Conservative    38;  Mismatches    71;  Indels    38;  Gaps   10;

Qy       18  EVATLSC----GHNVSVEELAQTRIYWQKEKKMVLTMM----SGDMNIWPEYKNRTIFDI  69
             |  |||     :|| ||   : || | |||||||:     :: ||||:|     : :: |
Db       34  ETADLPCQFANSQNQSLSELV---VFWQDQENLVLNEVYLGKEKFDSVHSKYMGRTSFD-  89

Qy       70  TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTS  129
             ::: :|:||:|||::|:|:||:      |  :|::|| :|  |: |
Db       90  SDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLANFSQPEI----VPIS  145

Qy      130  NIR----RIICSTSGGFPEP-HLSWLENGEELNAINTTV------SQDPETELYAVS     175
             |||      :|  |||||:|  |:||||||||:|||:||      :||||||| :|:
```

```
Db   146  NITENVYINLTCSSIHGYPEPKKMSVL-----LRTKNSTIEYDGIMQKSQDNVTELYDVS 200

Qy   176  SKLDF---NMTTNHSFMCLIKYGHLRV 199
               :|:|:|:| :|:::|:
Db   201  ISLSVSFPDVTSNMTIFCLLETDKTRL 227


RESULT 5
ICOL_HUMAN
ICOL_HUMAN
ID   ICOL_HUMAN     STANDARD;     PRT;     302 AA.
AC   O75144; Q9HD18; Q9NRQ1;
DT   15-JUL-1999 (Rel. 38, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
DE   (B7-related protein-1) (B7RP-1).
GN   ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Dendritic cell;
RX   MEDLINE=20477846; PubMed=11023515;
RA   Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
RT   "Costimulation of T cells by B7-H2, a B7-like molecule that binds
RT   ICOS.";
RL   Blood 96:2808-2813(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC   TISSUE=Peripheral blood lymphocytes;
RX   MEDLINE=20465019; PubMed=11007762;
RA   Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,
RA   Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,
RA   Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
RT   "Characterization of a new human B7-related protein: B7RP-1 is the
RT   ligand to the co-stimulatory protein ICOS.";
RL   Int. Immunol. 12:1439-1447(2000).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Leukocyte;
RX   MEDLINE=20126021; PubMed=10657606;
RA   Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA   Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,
RA   Jacobs K.A., Collins M.;
RT   "Identification of GL50, a novel B7-like protein that functionally
RT   binds to ICOS receptor.";
RL   J. Immunol. 164:1653-1657(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=9403880; PubMed=9734811;
RA   Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA   Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. X.
RT   The complete sequences of 100 new cDNA clones from brain which can
RT   code for large proteins in vitro.";
RL   DNA Res. 5:169-176(1998).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RA   Ling V., Dunussi-Joannopoulos K.;
RT   "G150 molecules and uses therefor.";
RL   Patent number WO0121796, 29-MAR-2001.
CC   -!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
CC       ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
CC       CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
CC       DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
CC       MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
CC       WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
CC       STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=O75144-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=O75144-2; Sequence=VSP_002520;
CC   -!- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
CC       KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE
CC       MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,
CC       SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN
CC       LYMPH NODES, LEUKOCYTES AND SPLEEN.
CC   -!- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
CC       TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
CC       MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC       SUBFAMILY.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- CAUTION: Ref.4 sequence differs from that shown in position 300
CC       onward for an unknown reason.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; AF199028; AAF34739.1; -.
DR   EMBL; AF289028; AAG01176.1; -.
DR   EMBL; AF216749; AAK16241.1; -.
DR   EMBL; AB014553; BAA31628.1; ALT_SEQ.
DR   EMBL; AX100595; CAC36465.1; -.
DR   MIM; 605717; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0003793; F:defense/immunity protein activity; NAS.
DR   GO; GO:0005102; F:receptor binding activity; TAS.
DR   GO; GO:0042104; P:positive regulation of activated T-cell pro...; TAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   GO; GO:0042110; P:T-cell activation; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR000047; ig; 2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   B-cell activation; Immune response; Glycoprotein;
KW   Immunoglobulin domain; Signal; Transmembrane; Multigene family;
KW   Alternative splicing.
FT   SIGNAL         1     18       POTENTIAL.
FT   CHAIN         19    302       ICOS LIGAND.
FT   DOMAIN        19    256       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     257    277       POTENTIAL.
FT   DOMAIN       278    302       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        19    129       IG-LIKE V-TYPE.
FT   DOMAIN       141    227       IG-LIKE C2-TYPE.
FT   DISULFID      37    113       POTENTIAL.
FT   DISULFID     158    216       POTENTIAL.
FT   CARBOHYD      70     70       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD     137    137       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD     173    173       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD     186    186       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   CARBOHYD     225    225       N-LINKED (GLCNAC...)  (POTENTIAL).
FT   VARSPLIC     300    302       GHV -> ESWNLLLLS (in isoform 2).
FT                                /FTId=VSP_002520.
SQ   SEQUENCE   302 AA;   33349 MW;   647934E21B55E34A CRC64;

Query Match     14.0%;  Score 161;  DB 1;  Length 302;
Best Local Similarity   26.4%;   Pred. No. 2.5e-06;
Matches   57;   Conservative  36;   Mismatches  95;   Indels  28;   Gaps   8;

Qy    14  KEVKEV---ATLSCG-HNVSVEELAQTRIYWQ-KEKKMVLT----MMSGDMNIWPEYKN 63
```

```
Db            |||:.:       |||
      23 KEVRAMVGSDVELSCACPEGSRFDLNDVYVVWQTSESKTVVTYHIPQNSSLENVDSRYRN 82
           |.|| |:  ::.||.. :|||: |:|| ||||:|
Qy    64 RTIFD---ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTP 119
           |.|:  |   .|:.||| :|||| |:||:
Db    83 RALMSPAGMLRGDFSLRLFNVTPQDEQKFHCLVLS-QSLGFQEVLSVEVTLHVAANFSVP 141

Qy   120 SISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETE--------L 171
           :|:| |: : ::::||||  .||||||||||| |
Db   142 VVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTD----NSLLDQALQNDTVFLNMRGL 196

Qy   172 YAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNT 207
           | .|::.||| ||||||||||||||
Db   197 YDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQT 232


RESULT 6
CD86_MOUSE
ID   CD86_MOUSE        STANDARD;      PRT;     309 AA.
AC   P42082;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE   antigen) (Early T cell costimulatory molecule-1) (ETC-1).
GN   CD86.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94065585; PubMed=7504059;
RA   Freeman G.J., Borriello F., Hodes R.J., Reiser H., Gribben J.G.,
RA   Ng J.W., Kim J., Goldberg J.M., Hathcock K., Laszlo G., Lombard L.A.,
RA   Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;
RT   "Murine B7-2, an alternative CTLA4 counter-receptor that costimulates
RT   T cell proliferation and interleukin 2 production.";
RL   J. Exp. Med. 178:2185-2192(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RX   MEDLINE=96094437; PubMed=7499829;
RA   Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
RT   "Differential expression of alternate mB7-2 transcripts.";
RL   J. Immunol. 155:5490-5497(1995).
RN   [3]
RP   SEQUENCE OF 7-309 FROM N.A.
RX   MEDLINE=94230971; PubMed=7513726;
RA   Chen C., Gault A., Shen L., Nabavi N.;
RT   "Molecular cloning and expression of early T cell costimulatory
RT   molecule-1 and its characterization as B7-2 molecule.";
RL   J. Immunol. 152:4929-4936(1994).
CC   -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC       FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN-2 PRODUCTION, BY
CC       BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC       EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC       SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CC       CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.
CC
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
```

```
DR   EMBL; L25606; AAA79770.1; -.
DR   EMBL; U39456; AAC52334.1; JOINED.
DR   EMBL; U39459; AAC52334.1; JOINED.
DR   EMBL; U39461; AAC52334.1; JOINED.
DR   EMBL; U39462; AAC52334.1; JOINED.
DR   EMBL; U39463; AAC52334.1; JOINED.
DR   EMBL; U39464; AAC52334.1; JOINED.
DR   EMBL; U39465; AAC52334.1; JOINED.
DR   EMBL; U39466; AAC52334.1; JOINED.
DR   EMBL; U39456; AAC52336.1; ALT_INIT.
DR   EMBL; U39461; AAC52336.1; JOINED.
DR   EMBL; U39463; AAC52336.1; JOINED.
DR   EMBL; U39464; AAC52336.1; JOINED.
DR   EMBL; U39465; AAC52336.1; JOINED.
DR   EMBL; U39466; AAC52336.1; JOINED.
DR   EMBL; S70108; AAB30744.2; ALT_INIT.
DR   PIR; I49522; I49522.
DR   MGD; MGI:101773; Cd86.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor.
FT   SIGNAL        1     23          POTENTIAL.
FT   CHAIN        24    309          T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT   DOMAIN       24    244          EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    245    265          POTENTIAL.
FT   DOMAIN      266    309          CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       33    128          IG-LIKE V-TYPE.
FT   DOMAIN      150    223          IG-LIKE C2-TYPE.
FT   DISULFID     40    110          POTENTIAL.
FT   DISULFID    157    216          POTENTIAL.
FT   CARBOHYD     33     33          N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     47     47          N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     92     92          N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    135    135          N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    146    146          N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    154    154          N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    175    175          N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    190    190          N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    231    231          N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   309 AA;  34665 MW;  8F58CD1FB81D5EA CRC64;

Query Match             13.2%;  Score 152;  DB 1;  Length 309;
Best Local Similarity   26.1%;  Pred. No. 1.4e-05;
Matches   52;  Conservative  43;  Mismatches  78;  Indels  26;  Gaps  10;

Qy    20 ATLSC---GHNVSVELAQTRIYWQKEKKMVL-----TMMSGDMNIWPEYKQNRTIFDI 69
            ||.|   :| |: |.||  :||| :|::||             ..|:::||
Db    36 AYLPCPFTKAQNISLSELV---VFWQDQQKLVLYEHYLGTEKLDSVN--AKYLGRTSFD- 89

Qy    70 TNNLSIVILALRPSDEGTYECVVLKYEK--DAFKREHLAEVTLSVKADFPTPSISDFEIP 127
            |.| :| .:||| :||||| |: :||:  |:|::||||:| |.|: :|:|::| :
Db    90 RNNWTLRLHNVQIKDMGSYDCFIQKKPPTGSIILQQTLTE--LSVIANFSEPEIKLAQNV 147

Qy   128 TSNIR-RIICSTSGGFPEPHLSW--LENGEELNAINTTVSQDPETELYAVSSKLDFNM-- 182
            |::|| |:|:: ||  :||::||    ::| |: || :::|::| |||||::|||:
Db   148 TGNSGINLTCTSKQGHPKPKKMYFLITNSTNEYGDNMQISQDNVTELFSISNSLSLSFPD 207

Qy   183 -TTNHSFMCLIKYGHLRVN 200
          .||| .:: .::.:|
Db   208 GVWHMTVVCVLETESMKIS 226


RESULT 7
ICOL_MOUSE
ID   ICOL_MOUSE        STANDARD;      PRT;     322 AA.
AC   Q9JHJ8;
DT   16-OCT-2001 (Rel. 40, Created)
```

```
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
DE   (B7-related protein-1) (B7RP-1) (LICOS).
GN   ICOSL OR B7H2 OR B7RP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC   TISSUE=Lymphocytes;
RX   MEDLINE=20083495; PubMed=10617205;
RA   Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
RA   Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tafuri-Bladt A.,
RA   Brankow D., Campbell P., Chang D., Chiu L., Dai T., Duncan G.,
RA   Elliott G.S., Hui A., McCabe S.M., Scully S., Shahinian A.,
RA   Shaklee C.L., Van G., Mak T.W., Senaldi G.;
RT   "T-cell co-stimulation through B7RP-1 and ICOS.";
RL   Nature 402:827-832(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Thymus;
RX   MEDLINE=20015817; PubMed=10549624;
RA   Swallow M.M., Wallin J.J., Sha W.C.;
RT   "B7h, a novel costimulatory homolog of B7.1 and B7.2, is induced by
RT   TNFalpha.";
RL   Immunity 11:423-432(1999).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=C3H/HeJ; TISSUE=Fetal thymus;
RX   MEDLINE=20126021; PubMed=10657606;
RA   Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA   Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,
RA   Jacobs K.A., Collins M.;
RT   "Identification of GL50, a novel B7-like protein that functionally
RT   binds to ICOS receptor.";
RL   J. Immunol. 164:1653-1657(2000).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Peripheral blood lymphocytes;
RX   MEDLINE=21286479; PubMed=11390480;
RA   Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finnerty H.F.,
RA   Collins M.;
RT   "Differential expression of inducible costimulator-ligand splice
RT   variants: lymphoid regulation of mouse g150-b and human g150
RT   molecules.";
RL   J. Immunol. 166:7300-7308(2001).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA   Ling V., Dunussi-Joannopolus K.;
RT   "G150 molecules and uses therefor.";
RL   Patent number WO0121796, 29-MAR-2001.
-!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
CC   ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
CC   CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
CC   DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
CC   MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
CC   WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
CC   STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION
CC   TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
CC   TH2 PHENOTYPE.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=2;
CC     Comment=Additional isoforms seem to exist;
CC   Name=1;
CC     IsoId=Q9JHJ8-1; Sequence=Displayed;
CC   Name=2; Synonyms=B;
CC     IsoId=Q9JHJ8-2; Sequence=VSP_002521;
-!- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
CC   TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
CC   (PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY

CC   FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PEYER'S
CC   PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY
CC   NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
CC   SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
CC   CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
CC   ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
-!- DEVELOPMENTAL STAGE: DETECTED EARLY IN HEMOPOIESIS: IN THE YOLK
CC   SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
CC   14.5 DPC.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC   SUBFAMILY.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed.  Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF216747; AAF45149.1; -.
DR   EMBL; AF199027; AAF34738.1; -.
DR   EMBL; AX100591; CAC36463.1; -.
DR   EMBL; AX100593; CAC36464.1; -.
DR   EMBL; AF394451; AAK77544.1; -.
DR   MGD; MGI:1354701; Icosl.
DR   GO; GO:0005576; C:extracellular; IDA.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0003793; F:defense/immunity protein activity; NAS.
DR   GO; GO:0005102; F:receptor binding activity; TAS.
DR   GO; GO:0045190; P:isotype switching; NAS.
DR   GO; GO:0042104; P:positive regulation of activated T-cell pro...; TAS.
DR   GO; GO:0045404; P:positive regulation of interleukin-4 biosyn...; IMP.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   GO; GO:0042110; P:T-cell activation; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   B-cell activation; Immune response; Glycoprotein;
KW   Immunoglobulin domain; Signal; Transmembrane; Multigene family;
KW   Alternative splicing.
FT   SIGNAL        1     46
FT   CHAIN        47    322       BY SIMILARITY.
FT   DOMAIN       47    277       ICOS LIGAND.
FT   TRANSMEM    278    298       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN      299    322       POTENTIAL.
FT   DOMAIN       49    149       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      167    263       IG-LIKE V-TYPE.
FT   DOMAIN       31     38       IG-LIKE C2-TYPE.
FT   DOMAIN      289    292       POLY-ALA.
FT   DISULFID     62    138       POLY-LEU.
FT   DISULFID    185    243       POTENTIAL.
FT   CARBOHYD     71     71       POTENTIAL.
FT   CARBOHYD    120    120       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    163    163       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    200    200       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    213    213       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    252    252       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    265    265       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC    321    322       HA -> TWAPVPYQDYLIPRYLMSPCLKTRGLP (in
FT                                isoform 2)
FT                                /FTId=VSP_002521.
FT   CONFLICT    237    237       R -> H (IN REF. 4 AND 5; CAC36464).
SQ   SEQUENCE   322 AA;  35960 MW;  55CCBA4AD12E47E6 CRC64;

Query Match             13.1%;  Score 150.5;  DB 1;  Length 322;
Best Local Similarity   27.1%;  Pred. No. 2e-05;
Matches  65;  Conservative  32;  Mismatches 102;  Indels  41;  Gaps  12;
```

```
FT   DOMAIN          33    127       IG-LIKE V-TYPE.
FT   DOMAIN         150    225       IG-LIKE C2-TYPE.
FT   DISULFID        40    110       POTENTIAL.
FT   DISULFID       157    218       POTENTIAL.
FT   CARBOHYD        33     33       N-LINKED (GLCNAC...    ) (POTENTIAL).
FT   CARBOHYD       135    135       N-LINKED (GLCNAC...    ) (POTENTIAL).
FT   CARBOHYD       146    146       N-LINKED (GLCNAC...    ) (POTENTIAL).
FT   CARBOHYD       154    154       N-LINKED (GLCNAC...    ) (POTENTIAL).
FT   CARBOHYD       177    177       N-LINKED (GLCNAC...    ) (POTENTIAL).
FT   CARBOHYD       192    192       N-LINKED (GLCNAC...    ) (POTENTIAL).
FT   CARBOHYD       198    198       N-LINKED (GLCNAC...    ) (POTENTIAL).
FT   CARBOHYD       213    213       N-LINKED (GLCNAC...    ) (POTENTIAL).
SQ   SEQUENCE       330 AA;  37142 MW;  935CDD65C57E3EE1 CRC64;

Query Match             12.2%;  Score 140.5;  DB 1;  Length 330;
Best Local Similarity   27.4%;  Pred. No. 0.00014;
Matches   60;  Conservative  34;  Mismatches  84;  Indels  41;  Gaps  12;

Qy    18  EVATLSCGH-NVSVEELAQTRIYWQKEKKMVLTMM----SGDMNIWPEYKNRTIFDITN-   71
                                                          :||| ::||||
Db    34  KTADLPCQFTNSQSRSLSELVVFWQDQERLVLYELFLGREKPDNVDPKYIGRTSFDQESW   93

Qy    72  NLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNI  131
          ||   :    ::| || |.|   ..||   | |::||| :|  |  |        ||
Db    94  NLQLHNVQIK--DKGVYQCFVHHRGAKGLVPIYQMNSELSVLANFTQPEIT----LISNI  147

Qy   132  RR-----IICSTSGGFPEPHLSWLENGEELNAINTTV----SQDPETELY-AVSS       176
                         |:||||||  |        |||       ||   |   ::
Db   148  TRNSAINLTCSSVQGYPEPKKMFF----VLKTENATTEYDGVIEKSQDNVTGLYNISISG  203

Qy   177  KLDF-NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFP                       214
                   :   :  ::  :      :|                  ::   |
Db   204  SITFSDDIRNATIYCVL------QTESTETYSQ-HFP                         233


RESULT 9
SHS1_RAT
ID   SHS1_RAT      STANDARD;      PRT;       509 AA.
AC   P97710; O08951; O70426; Q9QWI5;
DT   15-SEP-2003 (Rel. 42, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Protein-tyrosine phosphatase non-receptor type substrate 1 precursor
DE   (SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (Signal-
DE   regulatory protein alpha-1) (Sirp-alpha-1) (Brain Ig-like molecule
DE   with tyrosine-based activation motifs) (Bit) (Macrophage fusion
DE   receptor) (Macrophage membrane protein MFP150).
GN   PTPNS1 OR SHPS1 OR SIRP OR BIT OR MFR.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., SEQUENCE OF 42-60; 68-91; 128-137; 150-158;
RP   174-189; 192-202; 204-212; 218-237; 259-270; 279-282; 405-415 AND
RP   446-453, N-GLYCOSYLATION, PHOSPHORYLATION ON TYROSINE RESIDUES, AND
RP   INTERACTIONS WITH PTPN6 AND PTPN11.
RC   TISSUE=Fetal fibroblast;
RX   MEDLINE=97098667; PubMed=8943344;
RA   Fujioka Y., Matozaki T., Noguchi T., Iwamatsu A., Yamao T.,
RA   Takahashi N., Tsuda M., Takada T., Kasuga M.;
RT   "A novel membrane glycoprotein, SHPS-1, that binds the SH2-domain-
RT   containing protein tyrosine phosphatase SHP-2 in response to mitogens
RT   and cell adhesion.";
RL   Mol. Cell. Biol. 16:6887-6899(1996).
RN   [2]
RP   SEQUENCE FROM N.A., SEQUENCE OF 32-48 AND 446-453, FUNCTION, AND
RP   PHOSPHORYLATION ON TYROSINE RESIDUES.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=97415431; PubMed=9271230;
RA   Sano S.-I., Ohnishi H., Omori A., Hasegawa J., Kubota M.;
RT   "BIT, an immune antigen receptor-like molecule in the brain.";
RL   FEBS Lett. 411:327-334(1997).
```

```
Qy     2  LSHFC--SGVIHVTKEVKEVATLSCGHNVSVE------ELAQTRIYWQKEKKMV-----L   48
          |: :|     :|                 :||             ||.||.         :
Db    38  LSSLCAASAETEVGAMVGSNVVLSC------IDPHRRHFNLSGLYVYWQIENPEVSVTYYL   92

Qy    49  TMMSGDMNIWPEYKNRTIFDITN----NLSIVILALRPSDEGTYECVVLKYEKDAFKREH  104
          ||  |              |||    |||                 :|.||   ||   ||
Db    93  PYKSPGINVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRV--FMNTATELVK  150

Qy   105  LAE--VTLSVKADFPTP--SISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAIN  160
          |       :||||  |        :    |::            |:|     |:  ||.
Db   151  ILEEVVRLRVAANFSTPVISTSDSSNPGQE-RTYTCMSKNGYPENLYWI-NTTDNSLID   208

Qy   161  TTVSQDP----ETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVN------QTFNWNTTK   209
          ||.              :  ::|:     :    |||||||||||        :  |.
Db   209  TALQNNTVYLNKLGLYDVISTLRLPWTSRGDVLCCVENVALHQNITSISQAESFTGNNTK  268


RESULT 8
CD86_RABIT
ID   CD86_RABIT    STANDARD;      PRT;       330 AA.
AC   P42071;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   B lymphocyte activation antigen CD86 precursor (Activation B7-2
DE   antigen).
GN   CD86.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B/J X CHBB:HM;
RX   MEDLINE=95369849; PubMed=7642234;
RA   Isono T., Seto A.;
RT   "Cloning and sequencing of the rabbit gene encoding T-cell
RT   costimulatory molecules.";
RL   Immunogenetics 42:217-220(1995).
CC   -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC       FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC       BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC       EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC       SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CC       CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   --------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------
DR   EMBL; D49842; BAA08642.1; -.
DR   PIR; I46691; I46691.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW   Receptor.
FT   SIGNAL           1     22       POTENTIAL.
FT   CHAIN           23    330       B LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT   DOMAIN          23    247       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM       248    268       POTENTIAL.
FT   DOMAIN         269    330       CYTOPLASMIC (POTENTIAL).
```

```
RN   [3]
RP   SEQUENCE FROM N.A., SEQUENCE OF 99-107; 128-149; 192-217; 405-417;
RP   419-429; 446-467 AND 496-506, N-GLYCOSYLATION, AND TISSUE SPECIFICITY.
RC   STRAIN=Fischer 344; TISSUE=Macrophage;
RX   MEDLINE=98449911; PubMed=9774638;
RA   Saginario C., Sterling H., Beckers C., Kobayashi R., Solimena M.,
RA   Ullu E., Vignery A.;
RT   "MFR, a putative receptor mediating the fusion of macrophages.";
RL   Mol. Cell. Biol. 18:6213-6223(1998).
RN   [4]
RP   SEQUENCE OF 1-419 FROM N.A., AND TISSUE SPECIFICITY.
RC   STRAIN=WAG/Rij; TISSUE=Alveolar macrophage;
RX   MEDLINE=98375871; PubMed=9712053;
RA   Adams S., van der Laan L.J.W., Vernon-Wilson E.,
RA   Renardel de Lavalette C., Doepp E.A., Dijkstra C.D., Simmons D.L.,
RA   van den Berg T.K.;
RT   "Signal-regulatory protein is selectively expressed by myeloid and
RT   neuronal cells.";
RL   J. Immunol. 161:1853-1859(1998).
RN   [5]
RP   PHOSPHORYLATION IN RESPONSE TO EGF, AND INTERACTION WITH PTPN11.
RX   MEDLINE=98008865; PubMed=9344856;
RA   Ochi F., Matozaki T., Noguchi T., Fujioka Y., Yamao T., Takada T.,
RA   Tsuda M., Takeda H., Fukunaga K., Kasuga M.;
RT   "Epidermal growth factor stimulates the tyrosine phosphorylation of
RT   SHPS-1 and association of SHPS-1 with SHP-2, a SH2 domain-containing
RT   protein tyrosine phosphatase.";
RL   Biochem. Biophys. Res. Commun. 239:483-487(1997).
RN   [6]
RP   PHOSPHORYLATION OF TYR-477 AND TYR-501, AND MUTAGENESIS OF TYR-436;
RP   TYR-460; TYR-477 AND TYR-501.
RX   MEDLINE=99204923; PubMed=9535915;
RA   Takada T., Matozaki T., Takeda H., Fukunaga K., Noguchi T.,
RA   Fujioka Y., Okazaki I., Tsuda M., Yamao T., Ochi F., Kasuga M.;
RT   "Roles of the complex formation of SHPS-1 with SHP-2 in
RT   insulin-stimulated mitogen-activated protein kinase activation.";
RL   J. Biol. Chem. 273:9234-9242(1998).
CC   -!- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts
CC       as docking protein and induces translocation of PTPN6,
CC       PTPN11 and other binding partners from the cytosol to the
CC       plasma membrane. Supports adhesion of cerebellar neurons, neurite
CC       outgrowth and glial cell attachment. May play a key role in
CC       intracellular signaling during synaptogenesis and in synaptic
CC       function. Involved in the negative regulation of receptor tyrosine
CC       kinase-coupled cellular responses induced by cell adhesion, growth
CC       factors or insulin. Mediates negative regulation of phagocytosis,
CC       mast cell activation and dendritic cell activation. CD47 binding
CC       prevents maturation of immature dendritic cells and inhibits
CC       cytokine production by mature dendritic cells. May play a role in
CC       the release of nitric oxide by macrophages (By similarity).
CC   -!- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in
CC       macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro.
CC       Binds FGR. Binds JAK2 irrespective of its phosphorylation status
CC       and forms a stable complex. Binds SCAP1 and/or SCAP2. The
CC       resulting complex recruits FYB. Binds PTK2B (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain, spleen, lung, liver
CC       and kidney. Detected at lower levels in heart. Highly expressed in
CC       alveolar and peritoneal macrophages, and at lower levels in
CC       dendritic cells.
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: Phosphorylated on tyrosine residues in response to insulin,
CC       cell adhesion or epidermal growth factors. Dephosphorylated by
CC       PTPN11.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   --------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
```

```
CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; D85183; BAA12734.1; -.
DR   EMBL; D38468; BAA20368.1; -.
DR   EMBL; U62328; AAC68478.1; -.
DR   EMBL; AF055065; AAC18089.1; -.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00407; IGc1; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Repeat; Signal; Transmembrane; Immunoglobulin domain; SH3-binding;
KW   Glycoprotein; Phosphorylation.
FT   SIGNAL        1     31
FT   CHAIN        32    509       PROTEIN-TYROSINE PHOSPHATASE NON-RECEPTOR
FT                                TYPE SUBSTRATE 1.
FT   DOMAIN       28    394       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    374    394       POTENTIAL.
FT   DOMAIN      395    509       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       32    138       IG-LIKE V-TYPE.
FT   DOMAIN      150    248       IG-LIKE C1-TYPE 1.
FT   DOMAIN      255    349       IG-LIKE C1-TYPE 2.
FT   DISULFID     55    122       POTENTIAL.
FT   DISULFID    172    229       POTENTIAL.
FT   DISULFID    274    332       POTENTIAL.
FT   SITE        436    439       SH2-BINDING (POTENTIAL).
FT   SITE        446    451       SH3-BINDING (POTENTIAL).
FT   SITE        460    463       SH2-BINDING (POTENTIAL).
FT   SITE        477    480       SH2-BINDING (POTENTIAL).
FT   SITE        501    504       SH2-BINDING (POTENTIAL).
FT   MOD_RES     436    436       PHOSPHORYLATION (BY TYR-KINASES)
FT                                (POTENTIAL).
FT   MOD_RES     460    460       PHOSPHORYLATION (BY TYR-KINASES)
FT                                (POTENTIAL).
FT   MOD_RES     477    477       PHOSPHORYLATION (BY TYR-KINASES).
FT   MOD_RES     501    501       PHOSPHORYLATION (BY TYR-KINASES).
FT   CARBOHYD     54     54       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     93     93       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    169    169       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    181    181       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    205    205       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    209    209       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    242    242       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    246    246       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    271    271       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    293    293       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    312    312       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    320    320       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    345    345       N-LINKED (GLCNAC...) (POTENTIAL).
FT   MUTAGEN     436    436       Y->F: ABOLISHES TYROSINE PHOSPHORYLATION
FT                                AND PTPN11 BINDING; WHEN ASSOCIATED WITH
FT                                F-460, F-477 AND F-501.
FT   MUTAGEN     460    460       Y->F: ABOLISHES TYROSINE PHOSPHORYLATION
FT                                AND PTPN11 BINDING; WHEN ASSOCIATED WITH
FT                                F-436, F-477 AND F-501.
FT   MUTAGEN     477    477       Y->F: STRONGLY REDUCES INSULIN-INDUCED
FT                                TYROSINE PHOSPHORYLATION AND PTPN11
FT                                BINDING. ABOLISHES TYROSINE
FT                                PHOSPHORYLATION AND PTPN11 BINDING; WHEN
FT                                ASSOCIATED WITH F-436, F-460 AND F-501.
FT   MUTAGEN     501    501       Y->F: STRONGLY REDUCES INSULIN-INDUCED
FT                                TYROSINE PHOSPHORYLATION AND PTPN11
FT                                BINDING. ABOLISHES TYROSINE
FT                                PHOSPHORYLATION AND PTPN11 BINDING; WHEN
FT                                ASSOCIATED WITH F-436, F-460 AND F-477.
FT   CONFLICT      8      8       P -> L (IN REF. 4).
FT   CONFLICT     10     10       MISSING (IN REF. 4).
FT   CONFLICT     25     25       F -> I (IN REF. 3).
FT   CONFLICT     58     58       S -> C (IN REF. 4).
FT   CONFLICT     99    100       KR -> MP (IN REF. 3; AA SEQUENCE).
```

```
FT   CONFLICT     162    162       G -> A   (IN REF. 2).
FT   CONFLICT     189    189       D -> N.  (IN REF. 3).
FT   CONFLICT     205    205       N -> L   (IN REF. 3; AA SEQUENCE).
FT   CONFLICT     209    209       N -> S   (IN REF. 3; AA SEQUENCE).
FT   CONFLICT     405    405       G -> F   (IN REF. 3; AA SEQUENCE).
FT   CONFLICT     416    416       E -> P   (IN REF. 3; AA SEQUENCE).
FT   CONFLICT     418    421       NARE -> EGQN (IN REF. 3; AA SEQUENCE).
FT   CONFLICT     450    450       R -> E   (IN REF. 3; AA SEQUENCE).
FT   CONFLICT     499    499       MISSING  (IN REF. 3; AA SEQUENCE).
SQ   SEQUENCE   509 AA;  55690 MW;  5BE1FE0A4DD429F4 CRC64;

Query Match            12.0%;  Score 138;  DB 1;  Length 509;
Best Local Similarity  25.3%;  Pred. No. 0.00038;
Matches    75;  Conservative   36;  Mismatches   90;  Indels   96;  Gaps   20;

Qy    3  SHFCSGV------IHVTKEVKEV------ATLSCGHNVSVEELAQT-RIYWQK----EKKM   46
Db   23  SCFCAGASGKELKVTQADKSVSVAAGDSATLNC---TVSSLTPVGPIKWFKGEGQNRSP    78

Qy   47  VLTMMSGDMNIWPEYKNRTIFDIT--NNL-SIVILALRPSDEGTYECVVLKYEKDAFKR   102
Db   79  IYSFIGGEH--FPRITN--VSDATKRNMDFSICISNVTPEDAGTYYCV--KFQKGIVEP   132

Qy  103  EHLAEV------TLSVKADFPTPSIS--DFEIPTSNIRRIICSTSGGFPEP-HLSWLENG   153
Db  133  D--TEIKSGGGTTLYVLAKPSSPEVSGPDSRGSPGQTVNFTCKSYGFSPRNITLKWLKDG   190

Qy  154  EELNAINTTVSQDPETELYAVSSKLDFNMTTN--HS-FMCLIKYGHL-----------   197
Db  191  KELSHLETTISSKSNVS-YNISSTVSVKLSPEDIHSRVICEVAHVTLEGRPLNGTANFSN   249

Qy  198  ------------RVNQT-------------FNW---------NTTKQEHFPDN   216
Db  250  IIRVSPTLKITQQPLTPASQVNLTCQVQKFYPKALQLNWLENGNLSRTDKPEHFTDN   306


RESULT 10
C166_MOUSE
ID   C166_MOUSE      STANDARD;      PRT;   583 AA.
AC   Q61490; O70136;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE   (ALCAM) (DM-GRASP protein).
GN   ALCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NFS;
RX   MEDLINE=97535242; PubMed=9209500;
RA   Bowen M.A., Bajorath J., D'Egidio M., Whitney G.S., Palmer D.,
RA   Kobarg J., Starling G.C., Siadak A.W., Aruffo A.;
RT   "Characterization of mouse ALCAM (CD166): the CD6 binding domain is
RT   conserved in different homologs and mediates cross-species binding.";
RL   Eur. J. Immunol. 27:1469-1478(1997).
RN   [2]
RP   SEQUENCE OF 227-583 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=94376084; PubMed=8089660;
RA   Kanki J.P., Chang S., Kuwada J.Y.;
RT   "The molecular cloning and characterization of potential chick
RT   DM-GRASP homologs in zebrafish and mouse.";
RL   J. Neurobiol. 25:831-845(1994).
CC   -!- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
CC       NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
CC       INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
CC       ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
CC       THE NERVOUS SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
```

```
DR   EMBL; U95030; AAC06342.1; -.
DR   EMBL; L25274; AAA37528.1; -.
DR   HSSP; Q13740; 1KJC.
DR   MGD; MGI:1313266; Alcam.
DR   GO; GO:0019897; C:extrinsic to plasma membrane; IDA.
DR   GO; GO:0007165; P:signal transduction; IPI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 3.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal.
FT   SIGNAL         1     27       POTENTIAL.
FT   CHAIN         28    583       CD166 ANTIGEN.
FT   DOMAIN        28    527       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     528    549       POTENTIAL.
FT   DOMAIN       550    583       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        28    120       IG-LIKE V-TYPE 1.
FT   DOMAIN       125    234       IG-LIKE V-TYPE 2.
FT   DOMAIN       245    328       IG-LIKE C2-TYPE 1.
FT   DOMAIN       333    409       IG-LIKE C2-TYPE 2.
FT   DOMAIN       416    501       IG-LIKE C2-TYPE 3.
FT   DISULFID      43    113       POTENTIAL.
FT   DISULFID     157    220       POTENTIAL.
FT   DISULFID     270    313       POTENTIAL.
FT   DISULFID     354    392       POTENTIAL.
FT   DISULFID     435    485       POTENTIAL.
FT   CARBOHYD      95     95       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD     167    167       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD     265    265       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD     306    306       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD     361    361       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD     457    457       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD     480    480       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD     499    499       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CONFLICT     232    232       PSGQKT -> AAGIPA (IN REF. 2).
FT   CONFLICT     454    454       S -> F (IN REF. 2).
SQ   SEQUENCE   583 AA;  65161 MW;  E7BAFA8FCA8F9489 CRC64;

Query Match            11.7%;  Score 134.5;  DB 1;  Length 583;
Best Local Similarity  25.2%;  Pred. No. 0.00087;
Matches    38;  Conservative   34;  Mismatches   54;  Indels   25;  Gaps   7;

Qy   59  PEYKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPT   118
Db   84  PEYKDR--LSLSENYTLSIANAKISDEKRFVCMLVT-EDNVFEAPTLVKV------FKQ   133

Qy  119  PSISDFE------IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTVS------QD   166
Db  134  PSKPEIVNKAPFLETDQLKKLGDCISRDSYPDGNITWYRNGKVLQPVEGEVAILFKKEID   193

Qy  167  PETELYAVSSKLDFNMTTNH---SFMCLIKY   194
Db  194  PGTQLYTVTSSLEYKTTRSDIQMPFTCSVTY   224


RESULT 11
C166_HUMAN
ID   C166_HUMAN      STANDARD;      PRT;   583 AA.
```

```
AC   Q13740; O60892;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE   (ALCAM).
GN   ALCAM OR MEMD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95279947; PubMed=7760007;
RA   Bowen M.A., Patel D.D., Li X., Modrell B., Malacko A.R.,
RA   Wang W.-C., Marquardt H., Neubauer M., Pesando J.M., Francke U.,
RA   Haynes B.F., Aruffo A.;
RT   "Cloning, mapping, and characterization of activated leukocyte-cell
RT   adhesion molecule (ALCAM), a CD6 ligand.";
RL   J. Exp. Med. 181:2213-2220(1995).
RN   [2]
RP   SEQUENCE OF 2-583 FROM N.A.
RX   MEDLINE=98161527; PubMed=9502422;
RA   Degen W.G., van Kempen L.C., Gijzen E.G., van Groningen J.J.,
RA   van Kooyk Y., Bloemers H.P., Swart G.W.;
RT   "MEMD, a new cell adhesion molecule in metastasizing human melanoma
RT   cell lines, is identical to ALCAM (activated leukocyte cell adhesion
RT   molecule).";
RL   Am. J. Pathol. 152:805-813(1998).
RN   [3]
RP   CD6-BINDING DOMAINS.
RX   MEDLINE=96420463; PubMed=8823162;
RA   Skonier J.E., Bowen M.A., Emswiler J., Aruffo A., Bajorath J.;
RT   "Recognition of diverse proteins by members of the immunoglobulin
RT   superfamily: delineation of the receptor binding site in the human
RT   CD6 ligand ALCAM.";
RL   Biochemistry 35:12287-12291(1996).
RN   [4]
RP   3D-STRUCTURE MODELING OF 28-133.
RX   MEDLINE=96060095; PubMed=8520490;
RA   Bajorath J., Bowen M.A., Aruffo A.;
RT   "Molecular model of the N-terminal receptor-binding domain of the
RT   human CD6 ligand ALCAM.";
RL   Protein Sci. 4:1644-1647(1995).
CC   -!- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
CC       NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
CC       INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
CC       ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
CC       THE NERVOUS SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD166 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdi66.htm".
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; L38608; AAB53499.1; -.
DR   EMBL; Y10183; CAA71256.1; -.
DR   PIR; I39428; I39428.
DR   PDB; 1KJC; 03-APR-96.
DR   Genew; HGNC:400; ALCAM.
DR   MIM; 601662; -.
DR   GO; GO:0005102; F:receptor binding activity; TAS.
DR   GO; GO:0007155; P:cell adhesion; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 3.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Cell adhesion; Signal; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal; 3D-structure; Polymorphism.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    583       CD166 ANTIGEN.
FT   DOMAIN       28    527       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    528    549       POTENTIAL.
FT   DOMAIN      550    583       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       36    120       IG-LIKE V-TYPE 1.
FT   DOMAIN      125    234       IG-LIKE V-TYPE 2.
FT   DOMAIN      245    328       IG-LIKE C2-TYPE 1.
FT   DOMAIN      333    409       IG-LIKE C2-TYPE 2.
FT   DOMAIN      416    501       IG-LIKE C2-TYPE 3.
FT   DISULFID     43    113       POTENTIAL.
FT   DISULFID    157    220       POTENTIAL.
FT   DISULFID    270    313       POTENTIAL.
FT   DISULFID    354    392       POTENTIAL.
FT   DISULFID    435    485       POTENTIAL.
FT   CARBOHYD     91     91       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     95     95       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    167    167       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    265    265       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    306    306       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    361    361       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    457    457       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    480    480       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    499    499       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARIANT     258    258       N -> S.
FT                               /FTId=VAR_003907.
FT   VARIANT     301    301       M -> T.
FT                               /FTId=VAR_003908.
FT   STRAND       32     33
FT   STRAND       39     44
FT   STRAND       52     59
FT   TURN         61     62
FT   STRAND       65     71
FT   STRAND       76     78
FT   TURN         84     85
FT   STRAND       86     90
FT   STRAND       95    100
FT   STRAND      110    117
FT   TURN        118    119
FT   STRAND      120    123
FT   STRAND      127    128
FT   STRAND      130    131
SQ   SEQUENCE   583 AA;  65132 MW;  E023FB3974A60284 CRC64;
```

Query Match   11.6%; Score 133.5; DB 1; Length 583;
Best Local Similarity   24.5%; Pred. No. 0.0011;
Matches   37; Conservative   35; Mismatches   54; Indels   25; Gaps   7;

```
Qy       59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPT 118
            |||||  ||:| ::| ||  |  || ||| |   ||   :|  ||:::|  :| | |
Db       84 PEYKDR--LNLSENYTLSISNARISDEKRFVCMLVT-EDNVFEAPTIVKV------FKQ 133

Qy      119 PSISDFE-----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTV-----SQD 166
            |:|:   |       | :   |  ||| || ||| ::|:|  :    |:|        |:|
Db      134 PSKPEIVSKALFLETEQLKKLGDCISEDSYPDGNITWYRNGKVLHPLEGAVVIFKKEMD 193

Qy      167 PETELYAVSSKLDFNMT---TNHSFMCLIKY 194
            || ||  |::|:  :||
Db      194 PVTQLYTMTSTLEYKTTKADIQMPFTCSVTY 224
```

RESULT 12
BRF1_EBV
ID   BRF1_EBV   STANDARD;   PRT;   221 AA.
AC   P03228;

RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast;
RX   MEDLINE=9201696; PubMed=8611614;
RA   Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;
RT   "Cloning and sequence analysis of human butyrophilin reveals a
RT   potential receptor function.";
RL   Biochim. Biophys. Acta 1306:1-4(1996).
CC   -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC   MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC   ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC   MEMBRANE (BY SIMILARITY).
CC   -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC   (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC   SUBFAMILY.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; U39576; AAC50489.1; -.
DR   PIR; S70587; S70587.
DR   Genew; HGNC:1115; BTN1A1.
DR   MIM; 601610; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   InterPro; IPR001870; B302.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; IG_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   InterPro; IPR006574; PRY.
DR   InterPro; IPR003877; SPRY_receptor.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00622; SPRY; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00589; PRY; 1.
DR   SMART; SM00449; SPRY; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Repeat.
FT   SIGNAL   1   26   BY SIMILARITY.
FT   CHAIN   27   526   BUTYROPHILIN.
FT   DOMAIN   27   242   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   243   269   POTENTIAL.
FT   DOMAIN   270   526   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN   27   138   IG-LIKE V-TYPE 1.
FT   DOMAIN   148   234   IG-LIKE V-TYPE 2.
FT   CARBOHYD   55   55   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   215   215   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   526 AA; 59004 MW; E9ECA0CF8DAF94D5 CRC64;

Query Match   11.1%; Score 127; DB 1; Length 526;
Best Local Similarity   27.5%; Pred. No. 0.0032;
Matches   52; Conservative   33; Mismatches   84; Indels   20; Gaps   10;

Qy   16 VKEVATLSC--GHNVSVEELAQTRIYWQKEKKMVLTMMSG---DMNIWPEYKNRTIF--- 67
              ||:|:|:: ||::: ||||| || | || ||| :| ||||:| ||:
Db   42 VGEDAELPCRLSPNASAEHL-ELRWFRKKVSPAVLVHRDGREQEAEQMPEYRGRATLVQD 100

Qy   68 -DITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEI 126
               ::| ||:|||||| :| |:||:| :| ::: ||||:::   :||::| :: ::
Db   101 GIAKGRVALRIRGVRVSDDGEYTCF---FREDGSYEEAL--VHLKVAALGSDPHIS-MQV 154

Qy   127 PTSNIRRIICSTSGGFPEPHLSW-LENGEELNAINTTVSQDPETE-LYAVSSKLDFNMTT 184
              |||||||| ::|| || :| || ::|:|:: |:: :|:|:| :: |:
Db   155 QENGEICLECTSVGWYPEPQVQWRTSKGEKFP--STSESRNDEEGLFTVAASVIIRDTS 212

DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   33 kDa early protein (p33).
GN   BARF1.
OS   Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Gammaherpesvirinae; Lymphocryptovirus.
OX   NCBI_TaxID=10377;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84270667; PubMed=6087149;
RA   Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA   Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA   Tuffnell P.S., Barrell B.G.;
RT   "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL   Nature 310:207-211(1984).
RN   [2]
RP   IDENTIFICATION OF PROTEIN.
RX   MEDLINE=90059873; PubMed=2555151;
RA   Wei M.X., Ooka T.;
RT   "A transforming function of the BARF1 gene encoded by Epstein-Barr
RT   virus.";
RL   EMBO J. 8:2897-2903(1989).
CC   -!- FUNCTION: BARF1 HAS TRANSFORMING ACTIVITY.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; V01555; CAA24809.1; -.
DR   PIR; B43045; QQBE48.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Early protein; Oncogene.
FT   DOMAIN   1   120   IG-LIKE.
SQ   SEQUENCE   221 AA; 24471 MW; CA5A24D1EA28758E CRC64;

Query Match   11.2%; Score 129; DB 1; Length 221;
Best Local Similarity   27.0%; Pred. No. 0.00077;
Matches   43; Conservative   25; Mismatches   47; Indels   44; Gaps   8;

Qy   18 EVATLSCGHNVSVEELAQTRIYWQK------------EKKMVLTMMSGDMNIWPE 60
              ||:|:| |::::   :::|:: |: :|:
Db   19 QAVTAFLGERVTLTS----YWRRVSLGPEIEVSWFKLGPGEEQVLIGRMHHDV-IFIE 71

Qy   61 YKNRTIFDI---TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEV--TLSV-- 112
              |:||:| | | || | | :: | : |: |||||| ||||
Db   72 WPFRGFFDIHRSANTFLVVTAANISHDGNYLCRMKLGETEVTKQEHLSVVKPLTLSVHS 131

Qy   113 -KADFPTPSISDFEIPTSNIRRIICSTSGGFPEPHLSWL 150
                ||||||| :| ||:||| | |:|| || |: ||
Db   132 ERSQFP-----DFSVLT------VICTVNAFPHPHVQWL 159

RESULT 13
BUTY_HUMAN
ID   BUTY_HUMAN   STANDARD;   PRT;   526 AA.
AC   Q13410;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Butyrophilin precursor (BT).
GN   BTN1A1 OR BTN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;

```
. Qy      185  NHSFMCLIK 193
                    |:|:|
  Db      213  TKNVSCYIQ 221

RESULT 14
C166_CHICK
ID   C166_CHICK    STANDARD;      PRT;     588 AA.
AC   P42292;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   CD166 antigen precursor (SC1 glycoprotein) (BEN glycoprotein) (DM-
DE   GRASP protein) (JC7 protein).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 34-53.
RC   TISSUE=Embryo;
RX   MEDLINE=92030150; PubMed=1931049;
RA   Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,
RA   McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;
RT   "Molecular cloning and expression of a novel adhesion molecule, SC1.";
RL   Neuron 7:535-545(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91337449; PubMed=1873027;
RA   Burns F.R., von Kannen S., Guy L., Raper J.A., Kamholz J.,
RA   Chang S.;
RT   "DM-GRASP, a novel immunoglobulin superfamily axonal surface protein
RT   that supports neurite extension.";
RL   Neuron 7:209-220(1991).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582.
RC   TISSUE=Bursa of fabricius;
RX   MEDLINE=92302224; PubMed=1608932;
RA   Pourquie O., Corbel C., le Caer J.-P., Rossier J., le Douarin N.M.;
RT   "BEN, a surface glycoprotein of the immunoglobulin superfamily, is
RT   expressed in a variety of developing systems.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).
RN   [4]
RP   POSSIBLE FUNCTION.
RX   MEDLINE=92211411; PubMed=1313497;
RA   Pourquie O., Hallonet M.E.R., le Douarin N.M.;
RT   "Association of BEN glycoprotein expression with climbing fiber
RT   axonogenesis in the avian cerebellum.";
RL   J. Neurosci. 12:1548-1557(1992).
CC   -!- FUNCTION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING
CC       FIBER AXONOGENESIS. SUPPORTS NEURITE EXTENSION.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.
CC       WITHIN THE SPINAL CORD IT IS LOCALIZED TO AXONS IN THE DORSAL
CC       FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND IN
CC       EPITHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH
CC       DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS
CC       OF BEN.
CC   -!- DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC
CC       DEVELOPMENT.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; S63276; AAB20170.1; -.
DR   EMBL; M76678; AAA48602.1; -.
DR   EMBL; X64301; CAA45579.1; -.
DR   PIR; A45254; A45254.
DR   PIR; JH0464; JH0464.
DR   PIR; JH0506; JH0506.
DR   HSSP; Q13740; 1KJC.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 3.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal.
FT   SIGNAL        1     33
FT   CHAIN        34    588       CD166 ANTIGEN.
FT   DOMAIN       34    532       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    533    553       POTENTIAL.
FT   DOMAIN      554    588       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    126       IG-LIKE V-TYPE 1.
FT   DOMAIN      131    240       IG-LIKE V-TYPE 2.
FT   DOMAIN      251    333       IG-LIKE C2-TYPE 1.
FT   DOMAIN      338    414       IG-LIKE C2-TYPE 2.
FT   DOMAIN      421    501       IG-LIKE C2-TYPE 3.
FT   DISULFID     49    119       POTENTIAL.
FT   DISULFID    163    226       POTENTIAL.
FT   DISULFID    276    319       POTENTIAL.
FT   DISULFID    359    397       POTENTIAL.
FT   DISULFID    440    490       POTENTIAL.
FT   CARBOHYD    101    101       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    173    173       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    199    199       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    271    271       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    312    312       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    366    366       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    462    462       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    485    485       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD    504    504       N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CONFLICT      1     10       MEPPAAAAR -> MEPPSRRRP (IN REF. 3).
FT   CONFLICT     25     25       A -> S (IN REF. 3).
FT   CONFLICT    112    113       SD -> RH (IN REF. 3).
FT   CONFLICT    329    329       A -> T (IN REF. 2).
FT   CONFLICT    401    402       LQ -> HK (IN REF. 2).
SQ   SEQUENCE   588 AA;   65726 MW;  2A28612D0164531E CRC64;

Query Match             10.7%;  Score 122.5;  DB 1;  Length 588;
Best Local Similarity   25.7%;  Pred. No. 0.0087;
Matches     39;  Conservative   32;  Mismatches   54;  Indels  27;  Gaps   8;

Qy      59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
            |:||:||     |:||||||     |:||:|  :||| : || |||
Db      90 PDYKDR--LSLSENYTLSIKNARISDEKRFVCMLVT-EDDVSEEPTVVKV------FKQ 139

Qy     119 PS------ISDFEIPTSNIRRI-ICSTSGGFPEPHLSWLENG------EELNAINTTVSQ 165
                    |:||    ::||  |:|:|    :|||      ::||
Db     140 PSQPEILHQADF-LETEKLKMLGECVVRDSYPEGNVTWYKNGRVLQPVEEVVINLRKVE 198

Qy     166 DPETELYAVSSKLDFNMT---TNHSFMCLIKY 194
            |:|  | :||||  |       || ||||:|
Db     199 NRSTGLFTMTSSLQYMPTKEDANAKFTCIVTY 230

RESULT 15
SHS1_MOUSE
ID   SHS1_MOUSE    STANDARD;      PRT;     513 AA.
AC   P97797; O08907; O35924; O88555; O88556; P97796; Q8R559; Q9QX57;
AC   Q9WTN4;
DT   15-SEP-2003 (Rel. 42, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Protein-tyrosine phosphatase non-receptor type substrate 1 precursor
DE   (SHP substrate-1) (SHPS-1) (Inhibitory recepor SHPS-1) (Signal-
```

```
DE   regulatory protein alpha-1 (Sirp-alpha-1) (mSIRP-alpha) (MyD-1
DE   antigen) (Brain Ig-like molecule with tyrosine-based activation
DE   motifs) (Bit) (p84)
GN   PTPNS1 OR SHPS1 OR SIRP OR MYD1 OR BIT.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC   TISSUE=Brain;
RX   MEDLINE=97223399; PubMed=9070220;
RA   Yamao T., Matozaki T., Amano K., Matsuda Y., Takahashi N., Ochi F.,
RA   Fujioka Y., Kasuga M.;
RT   "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
RT   localization of genes.";
RL   Biochem. Biophys. Res. Commun. 231:61-67(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANTS ALA-29; ARG-67; ARG-91;
RP   THR-96; SER-128; PRO-194 AND ASN-224.
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=97230468; PubMed=9073522;
RA   Ohnishi H., Kubota M., Sano S.-I.;
RT   "BIT (Bit) maps to mouse chromosome 2.";
RL   Genomics 40:504-506(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), SEQUENCE OF 32-53 AND 422-433
RP   (ISOFORM 2), VARIANTS ALA-29, ARG-91; THR-96 AND SER-128,
RP   N-GLYCOSYLATION, AND TISSUE SPECIFICITY.
RC   STRAIN=BALB/c; TISSUE=Brain, and Cerebellum;
RX   MEDLINE=98012243; PubMed=348339;
RA   Comu S., Weng W., Olinsky S., Ishwad P., Mi Z., Hempel J., Watkins S.,
RA   Lagenaur C.F., Narayanan V.;
RT   "The murine P84 neural adhesion molecule is SHPS-1, a member of the
RT   phosphatase-binding protein family.";
RL   J. Neurosci. 17:8702-8710(1997).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), VARIANTS ALA-29; ARG-67;
RP   PRO-74; ALA-83; 86-TYR-VAL-87; ILE-90; ARG-91; THR-96; ALA-114;
RP   ILE-118; SER-128; PRO-194; ASN-224; PHE-351 AND ASP-365,
RP   N-GLYCOSYLATION, PHOSPHORYLATION ON TYROSINE RESIDUES, INTERACTION
RP   WITH PTPN6, AND TISSUE SPECIFICITY.
RC   STRAIN=C57BL/6; TISSUE=Fetal thymus;
RX   MEDLINE=98380500; PubMed=9712903;
RA   Veillette A., Thibaudeau E., Latour S.;
RT   "High expression of inhibitory receptor SHPS-1 and its association
RT   with protein tyrosine phosphatase SHP-1 in macrophages.";
RL   J. Biol. Chem. 273:22719-22728(1998).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), VARIANTS ALA-29; ARG-67;
RP   PRO-74; ALA-83; 86-TYR-VAL-87; ILE-90; ARG-91; THR-96; ALA-114;
RP   ILE-118; SER-128; PRO-194; ASN-224; PHE-351 AND ASP-365, AND
RP   N-GLYCOSYLATION.
RC   STRAIN=129/SvJ, and C57BL/6; TISSUE=Brain, and Liver;
RX   MEDLINE=20053880; PubMed=10585853;
RA   Sano S.-I., Ohnishi H., Kubota M.;
RT   "Gene structure of mouse BIT/SHPS-1.";
RL   Biochem. J. 344:667-675(1999).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORMS 2), AND VARIANTS ALA-29;
RP   PRO-74; ALA-83; 86-TYR-VAL-87; ILE-90; ARG-91; THR-96; ALA-114;
RP   ILE-118; SER-128; PRO-194; ASN-224; PHE-351 AND ASP-365.
RC   STRAIN=ILS, and ISS;
RX   MEDLINE=21363810; PubMed=11471062;
RA   Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA   Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT   "High-throughput sequence identification of gene coding variants
RT   within alcohol-related QTLs.";
RL   Mamm. Genome 12:657-663(2001).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT PRO-194.
RC   TISSUE=Placenta;
RA   Wang H., Chen Z., Ullrich A.;

RT   "Epidermal growth factor-induced association of SHP2 with mouse SIRP-
RT   alpha1.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX   MEDLINE=90152134; PubMed=2303162;
RA   Chuang W., Lagenaur C.F.;
RT   "Central nervous system antigen P84 can serve as a substrate for
RT   neurite outgrowth.";
RL   Dev. Biol. 137:219-232(1990).
RN   [9]
RP   N-GLYCOSYLATION, PHOSPHORYLATION BY JAK2 IN RESPONSE TO GROWTH
RP   HORMONE, AND INTERACTIONS WITH JAK2 AND PTPN11.
RX   MEDLINE=9817598; PubMed=9507023;
RA   Stofega M.R., Wang H., Ullrich A., Carter-Su C.;
RT   "Growth hormone regulation of SIRP and SHP-2 tyrosyl phosphorylation
RT   and association.";
RL   J. Biol. Chem. 273:7112-7117(1998).
RN   [10]
RP   INTERACTION WITH CD47, AND TISSUE SPECIFICITY.
RX   MEDLINE=99091586; PubMed=9872987;
RA   Jiang P., Lagenaur C.F., Narayanan V.;
RT   "Integrin-associated protein is a ligand for the P84 neural adhesion
RT   molecule.";
RL   J. Biol. Chem. 274:559-562(1999).
RN   [11]
RP   INTERACTION WITH FGR.
RX   MEDLINE=20130295; PubMed=10662797;
RA   Gresham H.D., Dale B.M., Potter J.W., Chang P.W., Vines C.M.,
RA   Lowell C.A., Lagenaur C.F., Willman C.L.;
RT   "Negative regulation of phagocytosis in murine macrophages by the Src
RT   kinase family member, Fgr.";
RL   J. Exp. Med. 191:515-528(2000).
CC   -!- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts
CC       as docking protein and induces translocation of PTPN6
CC       PTPN11 and other binding partners from the cytosol to the
CC       plasma membrane. Supports adhesion of cerebellar neurons, neurite
CC       outgrowth and glial cell attachment. May play a key role in
CC       intracellular signaling during synaptogenesis and in synaptic
CC       function. Involved in the negative regulation of receptor tyrosine
CC       kinase-coupled cellular responses induced by cell adhesion, growth
CC       factors or insulin. Mediates negative regulation of phagocytosis,
CC       mast cell activation and dendritic cell activation. CD47 binding
CC       prevents maturation of immature dendritic cells and inhibits
CC       cytokine production by mature dendritic cells (By similarity).
CC   -!- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in
CC       macrophages, where it primarily binds PTPN6. Binds GRB2 vitro.
CC       Binds FGR. Binds JAK2 irrespective of its phosphorylation status
CC       and forms a stable complex. Binds SCAP1 and/or SCAP2. The
CC       resulting complex recruits FYB. Binds PTK2B (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Comment=Additional isoforms seem to exist;
CC       Name=1; Synonyms=a;
CC         IsoId=P97797-1; Sequence=Displayed;
CC       Name=2; Synonyms=a', Large;
CC         IsoId=P97797-2; Sequence=VSP_007032;
CC       Name=3; Synonyms=b, Small;
CC         IsoId=P97797-3; Sequence=VSP_007031;
CC   -!- TISSUE SPECIFICITY: Highly expressed in cerebral cortex, brain,
CC       spinal cord, cerebellum, and spleen, and at much lower levels in
CC       kidney, thymus, heart, lung and liver. Within the cerebellum,
CC       highly expressed throughout the molecular layer, and in synaptic
CC       glomeruli in the granule cell layer. Detected in neurons of the
CC       hippocampus and dentate gyrus, and in olfactory bulb. Not detected
CC       in Purkinje cells. Highly expressed in the plexiform layers, optic
CC       fiber layer and the outer segments of the photoreceptor layer in
CC       the retina. Highly expressed in macrophages. Isoform 3 is detected
CC       at very low levels in all tissues tested.
CC   -!- DEVELOPMENTAL STAGE: Highly expressed in the CNS of embryos from
CC       day 7 to 17.
CC   -!- PTM: N-glycosylated.
```

```
CC   -!- PTM: Phosphorylated on tyrosine residues.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
```

```
DR   EMBL; D87967; BAA13520.1; -.
DR   EMBL; D87968; BAA13521.1; -.
DR   EMBL; D85785; BAA20376.1; -.
DR   EMBL; U89694; AAB92591.1; -.
DR   EMBL; AF072543; AAC24886.1; -.
DR   EMBL; AF072544; AAC24887.1; -.
DR   EMBL; AB024507; BAA89290.1; -.
DR   EMBL; AB024500; BAA89290.1; JOINED.
DR   EMBL; AB024501; BAA89290.1; JOINED.
DR   EMBL; AB024502; BAA89290.1; JOINED.
DR   EMBL; AB024503; BAA89290.1; JOINED.
DR   EMBL; AB024504; BAA89290.1; JOINED.
DR   EMBL; AB024505; BAA89290.1; JOINED.
DR   EMBL; AB024506; BAA89290.1; JOINED.
DR   EMBL; AB018194; BAA76555.1; -.
DR   EMBL; AB024507; BAA89289.1; -.
DR   EMBL; AB024500; BAA89289.1; JOINED.
DR   EMBL; AB024501; BAA89289.1; JOINED.
DR   EMBL; AB024502; BAA89289.1; JOINED.
DR   EMBL; AB024503; BAA89289.1; JOINED.
DR   EMBL; AB024504; BAA89289.1; JOINED.
DR   EMBL; AB024505; BAA89289.1; JOINED.
DR   EMBL; AB024506; BAA89289.1; JOINED.
DR   EMBL; AF332079; AAK56107.1; -.
DR   EMBL; AF332080; AAK56108.1; -.
DR   EMBL; Y10349; CAA71375.1; -.
DR   PIR; JC5289; JC5289.
DR   MGD; MGI:108563; Ptpns1.
DR   GO; GO:0008580; F:cytoskeletal regulator; IMP.
DR   GO; GO:0045309; F:phosphoprotein amino acid binding; IPI.
DR   GO; GO:0007015; P:actin filament organization; IMP.
DR   GO; GO:0006928; P:cell motility; IMP.
DR   GO; GO:0007160; P:cell-matrix adhesion; IMP.
DR   InterPro; IPR007110; Ig-like.
```

```
Query Match          10.5%;   Score 120.5; DB 1; Length 513;
Best Local Similarity 25.9%;   Pred. No. 0.011; DB 1;
Matches  59;   Conservative  42;   Mismatches  88;   Indels  39;   Gaps  15;

Qy     3 SHFCSGV------IHVTKEVKEVA------------TLSCGHNVSVEELAQTRIYWQK---EKKMVL 48
           :||||                :||:    |::|       |  |       :  ::::
Db    23 SCFCTGVTGKELKVTQPEKSVSVAAGDSTVLNC---TLTSLLPVGPIKWYRGVGQSRLLI 79

Qy    49 TMMSGDMNIWPEYKNRTIFDIT--NNL--SIVILALRPSDEGTYECVVLKYEKDAFKREH 104
           :||  |:|  || |||:|||      ||  ||||| |||||||||||:|||||||||||
Db    80 YSFTGEH--FPRVTN--VSDATKRNMDFSIRISNVTPEDAGTYYCV--KFQKGPSEPDT 133

Qy   105 L------AEVTLSVKADFPTPS-ISDFEIPTSNIRRIICSTSGGFPEP-HLSWLENGEEL 156
                  |:    |    |:|:||  |  |  | :       ||||| ::||:|
Db   134 EIQSGGGTEVYVLAKPSPPEVSGPADRGIPDQKV-NFTCKSHGFSPRNITLKWFKDGQEL 192

Qy   157 NAINTTVSQDPETELYAVSS--KLDFNMTTNHSFMCLIKYGHLRVNQT 202
           :: |||:    |:   :: :  ||   ||:    |||||||
Db   193 HHLETTVNPSGKNVSYNISSTVRVLNSMDVHS-KVICEVAHITLDRS 239
```

Search completed: November 25, 2003, 16:45:48
Job time : 42 secs

THIS PAGE BLANK (USPTO)

OM protein - protein search, using sw model

Copyright GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: November 25, 2003, 16:42:47 ; Search time 35 Seconds
(without alignments)
1592.553 Million cell updates/sec

Title: US-09-666-267B-8
Perfect score: 1149
Sequence: 1 GLSHFCSGVIHVTKEVKEVA.........LRVNQTFNWNTTKQEHFPDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Match Length	DB	ID	Description
1	1118	97.3	288	6	O77684	O77684 macaca neme
2	1100	95.7	288	6	Q28499	Q28499 macaca mula
3	1085	94.4	288	6	Q9BDN6	Q9BDN6 cercocebus
4	1085	94.4	289	6	Q28347	Q28347 cercocebus
5	772	67.2	296	6	Q8WMZ2	Q8WMZ2 sus scrofa
6	764	66.5	230	6	Q9N2I3	Q9N2I3 sus scrofa
7	762.5	66.4	288	6	Q9TT70	Q9TT70 sus scrofa
8	762.5	66.4	288	6	Q9BE99	Q9BE99 sus scrofa
9	761	66.2	297	6	Q9TT71	Q9TT71 sus scrofa
10	743	64.7	292	6	Q9GMZ8	Q9GMZ8 felis silve
11	743	64.7	292	6	O02758	O02758 felis silve
12	719	62.6	304	6	Q9TQX1	Q9TQX1 canis famil
13	717.5	62.4	296	6	O46405	O46405 bos taurus
14	705	61.4	235	6	Q9N0T0	Q9N0T0 canis famil
15	705	61.4	235	6	Q9TQS8	Q9TQS8 canis famil
16	659	57.4	294	11	Q8BH36	Q8BH36 mesocricetu
17	603.5	52.5	321	11	O35187	O35187 rattus norv
18	602	52.4	290	11	Q62680	Q62680 rattus norv
19	601.5	52.3	321	11	Q62624	Q62624 rattus norv
20	596	51.9	321	11	O55202	O55202 rattus norv
21	560	48.7	306	11	Q9R1Z9	Q9R1Z9 mus musculu
22	560	30.5	174	6	Q9GMZ9	Q9GMZ9 felis silve
23	349.5	30.4	173	6	Q95L17	Q95L17 felis silve
24	255.5	22.2	212	11	Q61332	Q61332 mus musculu
25	200.5	17.4	329	6	Q9XSX6	Q9XSX6 felis silve
26	200.5	17.4	332	6	Q9GMZ7	Q9GMZ7 felis silve
27	200.5	17.4	332	6	Q95L16	Q95L16 felis silve
28	188.5	16.4	280	6	Q9TTF1	Q9TTF1 canis famil
29	188.5	16.4	296	13	O42404	O42404 gallus gall
30	182	15.8	329	6	Q9TTF2	Q9TTF2 cercopithec
31	178	15.5	323	6	Q9BDM2	Q9BDM2 cercopithec
32	177	15.4	323	6	Q9BDM9	Q9BDM9 macaca neme
33	177	15.4	323	6	Q9BDM4	Q9BDM4 macaca mula
34	176	15.3	275	6	Q9BDN9	Q9BDN9 papio anubi
35	176	15.3	323	6	Q9BDB8	Q9BDB8 cercocebus
36	171	14.9	284	6	Q9GL33	Q9GL33 bos taurus
37	166.5	14.5	289	11	Q8K3J3	Q8K3J3 meriones un
38	165	14.4	281	11	Q8CJE8	Q8CJE8 mesocricetu
39	162	14.1	313	11	O35531	O35531 rattus norv
40	161.5	14.1	325	6	O02838	O02838 sus scrofa
41	159	13.8	316	11	Q8VE98	Q8VE98 mus musculu
42	156.5	13.6	290	4	Q9NZQ7	Q9NZQ7 homo sapien
43	153	13.3	290	11	Q9EP73	Q9EP73 mus musculu
44	153	13.3	356	11	Q64381	Q64381 mus musculu
45	152	13.2	314	11	Q61238	Q61238 mus musculu

ALIGNMENTS

RESULT 1
O77684
ID   O77684   PRELIMINARY;   PRT;   288 AA.
AC   O77684;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   B7 protein.
GN   B7.
OS   Macaca nemestrina (Pig-tailed macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9545;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kraus G., Hnatyszyn J.H.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF079519; AAC31555.1; -.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   288 AA;   33131 MW;   76BBC42839E9AB79 CRC64;

Query Match   97.3%;
Best Local Similarity   97.7%;
Matches 210; Conservative   1; Mismatches   4; Indels   0; Gaps   0;

Score 1118;   DB 6;   Length 288;
Pred. No. 1e-92;

Qy   2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMSGDMNIWPEY 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMSGDMNIWPEY 87

Qy   62 KNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88 KNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVMLSVKADFPTPSI 147

```
Qy    122  SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
           :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148  TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYTVSSKLDFN 207

Qy    182  MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
           |||||||||||||||||||||||||||||||||||
Db    208  MTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFPDN 242
```

RESULT 2
Q28499
ID   Q28499;   PRELIMINARY;   PRT;   288 AA.
AC   Q28499;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   B7 protein (CD80 protein precursor).
GN   B7 OR N939.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 0:0-0(2001).
DR   EMBL; U19840; AAA86706.1; -.
DR   EMBL; AF344849; AAK37609.1; -.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Signal.
FT   SIGNAL   1   26   POTENTIAL.
SQ   SEQUENCE   288 AA; 33141 MW; E70BEA4006C7A609 CRC64;

Query Match   95.7%; Score 1100; DB 6; Length 288;
Best Local Similarity   96.3%; Pred. No. 4.2e-91;
Matches 207; Conservative   2; Mismatches   6; Indels   0; Gaps   0;

```
Qy      2  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     28  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 87

Qy     62  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
.Db    88  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSI 147

Qy    122  SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
           :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148  TDSEIPPSNIRRIICSNSGGFPEPHLSWLENGEELNAISTTVSQDPETELYTVSSKLDFN 207

Qy    182  MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
           |||||||||||||||||||||||||||||||||||
Db    208  MTTNHSFMCLIKYGHLRVNQTFNWNTPKQEHFPDN 242
```

RESULT 3
Q9BDN6
ID   Q9BDN6   PRELIMINARY;   PRT;   288 AA.
AC   Q9BDN6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   CD80 protein.
GN   MNB71.
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21383618; PubMed=11491535;
RA   Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
DR   EMBL; AF344839; AAK37535.1; -.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   288 AA; 32917 MW; C6A3F6A3C92972B CRC64;

Query Match   94.4%; Score 1085; DB 6; Length 288;
Best Local Similarity   95.3%; Pred. No. 9.4e-90;
Matches 205; Conservative   4; Mismatches   6; Indels   0; Gaps   0;

```
Qy      2  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMSGDMNIWPEY 61
           |||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db     28  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYCQKEKKMVLTMISGDMNIWPEY 87

Qy     62  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVMLSVKADFPTPSI 147

Qy    122  SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
           :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148  TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGGELNAIDTTVSQDPETELYTVSSKLDFN 207

Qy    182  MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
           |||||||:|||||||||||||||||||||||||||
Db    208  MTTNHSFVCLIKYGHLRVNQTFNWNTPKQEHFPDN 242
```

RESULT 4
Q28347
ID   Q28347;   PRELIMINARY;   PRT;.   289 AA.
AC   Q28347;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   B7 protein (Fragment).
GN   B7.
OS   Cercocebus torquatus (red-crowned mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and

```
RT   nonhuman primates ";
RL   J. Immunol. 155:3946-3954(1995).
DR   EMBL; U19833; AAA86700.1; -.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      289    289
SQ   SEQUENCE   289 AA;  33030 MW;  5ED6A3F6A3C59297 CRC64;

Query Match             94.4%;  Score 1085;  DB 6;  Length 289;
Best Local Similarity   95.3%;  Pred. No. 9.5e-90;
Matches  205;  Conservative   4;  Mismatches   6;  Indels   0;  Gaps   0;

Qy      2  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY  61
           |||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db     28  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYCQKEKKMVLTMISGDMNIWPEY  87

Qy     62  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 147

Qy    122  SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
           :||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db    148  TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGEELNAIDTTVSQDPETELYTVSSKLDFN 207

Qy    182  MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
           ||||||||:|||||||||||||||||||||||||
Db    208  MTTNHSFVCLIKYGHLRVNQTFNWNTPKQEHFPDN 242

RESULT 5
Q8WMZ2
ID   Q8WMZ2;      PRELIMINARY;      PRT;   296 AA.
AC   Q8WMZ2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   CD80.
GN   CD80.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tadaki D.K., Williams A., Lee K.P., Kirk A.D., Harlan D.M.;
RT   "Porcine CD80: Cloning, characterization and evidence for its role in
RT   direct human T-cell activation.";
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF455811; AAL58443.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   296 AA;  33275 MW;  69E494237E679C98 CRC64;

Query Match             67.2%;  Score 772;  DB 6;  Length 296;
Best Local Similarity   66.8%;  Pred. No. 1.6e-61;
Matches  141;  Conservative  28;  Mismatches  42;  Indels   0;  Gaps   0;

Qy      1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  60
           ||| ||||| |||| ||:|| :|| ||| |||||||:||||||:| ||||::||
Db     22  GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK  81

Qy     61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
           |:||||| |:||| |||||||| || |||||||:|| :::|| :||||:||||||||||
Db     82  YENRTFTDVTNNLCIVILALRLSDNGTYTCVVQKRERGSYKLEHLTSVKLMVKADFPVPS 141
```

```
Qy    121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
           :| : |||:|||:|||||||||||||||||||||||||| :||:||||||||::|| |
Db    142  ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF 201

Qy    181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQE 211
           : | ||||||||:|||: ||| ||||| :|:
Db    202  NVTGNHSFMCLVKYGGLTVSQTFNWQKSKRE 232

RESULT 6
Q9N2I3
ID   Q9N2I3;      PRELIMINARY;      PRT;   230 AA.
AC   Q9N2I3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   CD80 protein precursor.
GN   CD80/B7.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Landrace; TISSUE=Spleen;
RA   Wada M., Amae S., Hoshi M., Nio M., Ohi R.;
RT   "Porcine CD80(B-7) mRNA, partial cds.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB026121; BAA90700.2; -.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   signal.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    230       POTENTIAL.
SQ   SEQUENCE   230 AA;  26028 MW;  EB63AD172663C4A4 CRC64;

Query Match             66.5%;  Score 764;  DB 6;  Length 230;
Best Local Similarity   67.0%;  Pred. No. 6.2e-61;
Matches  140;  Conservative  26;  Mismatches  43;  Indels   0;  Gaps   0;

Qy      1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  60
           ||| ||||| |||| ||:|| :|| ||| |||||||:||||||:| ||||::||
Db     22  GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK  81

Qy     61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
           |:||||| |:||| |||||||| || |||||||:|| :::|| :||||:||||||||||
Db     82  YENRTFTDVTNNLCIVILALRLSDNGTYTCVVQKRERGSYKLEHLTSVKLMVKADFPVPS 141

Qy    121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
           :| : |||:|||:|||||||||||||||||||||||||| :||:||||||||::|| |
Db    142  ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF 201

Qy    181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTK 209
           : | ||||||||:|||: ||| |||||
Db    202  NVTGNHSFMCLVKYGGLTVSQTFNWQCCK 230

RESULT 7
Q9TT70
ID   Q9TT70;      PRELIMINARY;      PRT;   288 AA.
AC   Q9TT70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   CD80 protein precursor (Fragment).
GN   CD80.
OS   Sus scrofa (Pig).
```

OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20302785; PubMed=10843688;
RA   Faas S.J., Giannoni M.A., Mickle A., Kiesecker C.L., Reed D.J., Wu D.,
RA   Fodor W.L., Mueller J.P., Matis L.A., Rother R.P.;
RT   "Primary Structure and Functional Characterization of a Soluble,
RT   Alternatively Spliced Form of B7-1.";
RL   J. Immunol. 164:6340-6348(2000).
DR   EMBL; AF203443; AAF22750.1; -.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Signal.
FT   SIGNAL   1   29
FT   CHAIN   30   >288
FT   NON_TER   288   288
SQ   SEQUENCE   288 AA; 32510 MW; 67E31D0FDB45D1C8 CRC64;

Query Match   66.4%; Score 762.5; DB 6; Length 288;
Best Local Similarity   66.5%; Pred. No. 1.1e-60;
Matches 141; Conservative   28; Mismatches   42; Indels   1; Gaps   1;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
              ||||||||:||:||||||||||||||:.:|||:::|||:::::||||:.:|||:||||||
Db   22 GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK 81

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
              |:|||||||||||||||||||||||||||||||||:||:::||||||:::||||||||||
Db   82 YENRFTFDVTNNLCIVILALRLSDNGTYTCVVQKRERGSYKLEHLTSVKLMVKADFPVPS 141

Qy   121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
              ||||:||||:|||:||||||||||||||||||||||:|||||||||||||||:|||||||
Db   142 ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF 201

Qy   181 NMTTNHSFMCLIKYGHLRVNQTFNW-NTTKQE 211
              :|||||||||||||||||||||||| :|:|
Db   202 NVTGNHSFMCLVKYGGLTVSQTFNWQKSAKRE 233

RESULT 8
Q9BE99
ID   Q9BE99;   PRELIMINARY;   PRT;   297 AA.
AC   Q9BE99;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   CD80 protein precursor.
GN   CD80/B7-1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Landrace; TISSUE=Ileal mucosa;
RA   Wada M., Amae S., Sano N., Ishii T., Hoshi M., Sasaki H., Nio M.,
RA   Hayashi Y., Ohi R.;
RT   "cloning and sequencing of cDNAs for porcine B7-1 (CD80) and soluble
RT   isoforms.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB049760; BAB40952.1; -.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Signal.
FT   SIGNAL   1   29   POTENTIAL.
FT   CHAIN   30   297   CD80 PROTEIN.
SQ   SEQUENCE   297 AA; 33438 MW; 23109711EA63EF23 CRC64;

Query Match   66.4%; Score 762.5; DB 6; Length 297;
Best Local Similarity   66.5%; Pred. No. 1.2e-60;
Matches 141; Conservative   28; Mismatches   42; Indels   1; Gaps   1;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
              ||||||||:||:||||||||||||||:.:|||:::|||:::::||||:.:|||:||||||
Db   22 GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK 81

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
              |:|||||||||||||||||||||||||||||||||:||:::||||||:::||||||||||
Db   82 YENRFTFDVTNNLCIVILALRLSDNGTYTCVVQKRERGSYKLEHLTSVKLMVKADFPVPS 141

Qy   121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
              ||||:||||:|||:||||||||||||||||||||||:|||||||||||||||:|||||||
Db   142 ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF 201

Qy   181 NMTTNHSFMCLIKYGHLRVNQTFNW-NTTKQE 211
              :|||||||||||||||||||||||| :|:|
Db   202 NVTGNHSFMCLVKYGGLTVSQTFNWQKSAKRE 233

RESULT 9
Q9TT71
ID   Q9TT71;   PRELIMINARY;   PRT;   229 AA.
AC   Q9TT71;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   CD80 OR CD80/B7-1.
GN   CD80 OR CD80/B7-1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Faas S.J., Giannoni M.A., Mickle A., Kiesecker C.L., Reed D.J., Wu D.,
RA   Fodor W.L., Meuller J.P., Matis L.A., Rother R.P.;
RT   "Primary Structure and Functional Characterization of a Soluble,
RT   Alternatively Spliced Form of B7-1.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Wada M., Amae S., Hoshi M., Nio M., Ishii T., Sano N., Sasaki H.,
RA   Ohi R.;
RT   "Splicing Isoform of Porcine CD80.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF203442; AAF22749.1; -.
DR   EMBL; AB038153; BAA90764.1; -.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Signal.
FT   SIGNAL   1   29
FT   CHAIN   30   229
SQ   SEQUENCE   229 AA; 25900 MW; C3AD172663C4A4ED CRC64;

Query Match   66.2%; Score 761; DB 6; Length 229;
Best Local Similarity   67.8%; Pred. No. 1.1e-60;
Matches 139; Conservative   26; Mismatches   40; Indels   0; Gaps   0;

Qy   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
              |||||| |||||||||||||||| ||| |||||||:||:||||:||| : ||||
Db   22 GLFDFCSGIVQVTKTVKEIAVLSCDYNISTKELTRVRIYWQKDNEMVLAVMSGKVVWPK 81

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
              |:|||||||||||:|||||||||||||| ||||||:|||: :| ||||||||||||
Db   82 YENRFTFDVTNNLCIVILALRLSDNGTYTCVVQKRERGSYKLEHLTSVKLMVKADFPVPS 141

Qy   121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
              |: :||:||||||||||||||||||||||||||||:|||||||||||||||:|||||
Db   142 ITALGNPSPNIKRIRCSTSGGFPEPHLSWLENGEELNATNTMLSQDPETELYMISSELDF 201

Qy   181 NMTTNHSFMCLIKYGHLRVNQTFNW 205
              |:|||||||||||||| :||||||
Db   202 NVTGNHSFMCLVKYCGGLTVSQTFNW 226

RESULT 10
Q9GMZ8
ID   Q9GMZ8   PRELIMINARY;   PRT;   292 AA.
AC   Q9GMZ8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   B-lymphocyte activation antigen B7-1 (CD80).
GN   CD80.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20485322; PubMed=11029611;
RA   Nishimura Y., Shinojima M., Miyazawa T., Sato E., Nakamura K.,
RA   Izumiya Y., Ikeda Y., Mikami T., Takahashi E.;
RT   "Molecular cloning of the cDNA encoding the feline B-lymphocyte
RT   activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which
RT   interact with human CTLA4-Ig.";
RL   Eur. J. Immunogenet. 27:427-430(2000).
DR   EMBL; AB030651; BAB11687.1; -.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   292 AA;   33540 MW;   ED9AEECE10D30401 CRC64;

Query Match   64.7%;   Score 743;   DB 6;   Length 292;
Best Local Similarity   63.3%;   Pred. No. 6.5e-59;
Matches 136;   Conservative 33;   Mismatches 44;   Indels 2;   Gaps 1;

Qy   2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
              :||||||| || ||:||| |||| || ||| | ||||||||: || ::||:|
Db   28 LFYFCSGIIQVNKTVEEVAVLSCDYNISTKELTEIRIYWQKDDEMVLAVMSGKVQVWPKY 87

Qy   62 KNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
              |||| ||:||| ||||||| |:|||| |: | : |||||| :|||||||||| |||
Db   88 KNRTFTDVTDNHSIVIMALRLSDNGKYTCIIQKIEKGSYKVKHLTSVMLLVRADFPVPSI 147

Qy   122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||:|||
Db   148 TDLGNPSHNIKRIMCLTSGGFPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDFN 207

Qy   182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
              |||||||||||| |||||||||||| |: ||||
Db   208 MTNNHSFLCLVKYGNLLVSQIFNWQ--KSEPQPSN 240

RESULT 11
O02758
ID   O02758   PRELIMINARY;   PRT;   292 AA.
AC   O02758;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   T-cell specific surface glycoprotein B7-1.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hash S.M., Collisson E.W.;
RT   "Felis catus t-cell specific surface glycoprotein B7-1.";
RL   Thesis (1996), Veterinary Pathobiology, Texas A&M Univ.
DR   EMBL; U57755; AAB53575.1; -.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   292 AA;   33482 MW;   6F117E7852B79S0F CRC64;

Query Match   64.7%;   Score 743;   DB 6;   Length 292;
Best Local Similarity   63.3%;   Pred. No. 6.5e-59;
Matches 136;   Conservative 33;   Mismatches 44;   Indels 2;   Gaps 1;

Qy   2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
              :||||||| || ||:|||||| |||| || ||| | ||||||||: || ::||:|
Db   28 LFYFCSGIIQVNKTVEEVAVLSCDYNISTKELTEIRIYWQKDDEMVLAVMSGKVQVWPKY 87

Qy   62 KNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
              |||| ||:||| ||||||| |:|||| |: | : |||||| :|||||||||| |||
Db   88 KNRTFTDVTDNHSIVIMALRLSDNGKYTCIIQKIEKGSYKVKHLTSVMLLVRADFPVPSI 147

Qy   122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||:|||
Db   148 TDLGNPSHNIKRIMCLTSGGFPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDFN 207

Qy   182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
              |||||||||||| |||||||||||| |: ||||
Db   208 MTNNHSFLCLVKYGNLLVSQIFNWQ--KSEPQPSN 240

RESULT 12
Q9TQX1
ID   Q9TQX1   PRELIMINARY;   PRT;   304 AA.
AC   Q9TQX1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   B7-1 protein precursor.
GN   CD80.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20093996; PubMed=10630300;
RA   Yang S., Sim G.-K.;
RT   "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
RT   Molecules.";
RL   Immunogenetics 50:349-353(1999).
DR   EMBL; AF106824; AAF17295.1; -.
DR   EMBL; AF106833; AAF17293.1; -.
DR   EMBL; AF106829; AAF17293.1; JOINED.
DR   EMBL; AF106830; AAF17293.1; JOINED.
DR   EMBL; AF106831; AAF17293.1; JOINED.
DR   EMBL; AF106832; AAF17293.1; JOINED.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.

```
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; IG; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Signal.
FT   SIGNAL          1      33       POTENTIAL.
FT   CHAIN          34     304       B7-1 PROTEIN.
SQ   SEQUENCE      304 AA;  34454 MW;  09E082F6BB06C94F CRC64;

Query Match             62.6%;  Score 719;  DB 6;  Length 304;
Best Local Similarity   60.5%;  Pred. No. 1e-56;
Matches  130;  Conservative  36;  Mismatches  49;  Indels   0;  Gaps   0;

Qy        2  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY   61
                :|||||:||:|||||||||||||||  : :| :||||||  :|:||  :| | |||||
Db       28  LFYFCSGIIQVNKTVKEVAVLSCDYNISTTELMKVRIYWQKDDEVVLAVTSGQTKVWSKY   87

Qy       62  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI  121
             ::| |||||||||||||||||||:|||||| ::| :|| : :|:: ||||::||||
Db       88  ENRTFADFTNNLSIVIMALRLSDNGKYTCIVQKTEKRSYKVKHMTSVMLLVRADFPVPSI  147

Qy      122  SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN  181
                ||||||||||||||||||||:||||||||||||: |||||||  :|||:| |::
Db      148  TDLGNPSHDIKRIMCSTSGGFPKPHLSWWENEEELNAANTTVSQDPDTELYTISSELDFN  207

Qy      182  MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  216
             :|:|||:||||||||||| :||:||:| ::|:|
Db      208  ITSNHSFVCLVKYGDLTVSQIFNWQKSVEPHPPNN  242


RESULT 13
O46405
ID   O46405       PRELIMINARY;       PRT;   296 AA.
AC   O46405;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   CD80 anitgen precursor (Fragment)
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99115507; PubMed=9914337;
RA   Parsons K.R., Howard C.J.;
RT   "Cloning of cattle CD80.";
RL   Immunogenetics 49:231-234(1999).
DR   EMBL; Y09950; CAA71081.1; -.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Signal.
FT   SIGNAL          1      25       POTENTIAL.
FT   NON_TER       296     296
SQ   SEQUENCE      296 AA;  33618 MW;  7ADB11FB5F532EF5 CRC64;

Query Match             62.4%;  Score 717.5;  DB 6;  Length 296;
Best Local Similarity   63.2%;  Pred. No. 1.3e-56;
Matches  134;  Conservative  28;  Mismatches  47;  Indels   3;  Gaps   2;

Qy        1  GLSHFCSGVI--HVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIW   58
             |:||||:|:    :|||||||||| :  :|:||||||||||||  : |||| ||| |
Db       27  GLFYFCSGITPKSVTKRVKEFVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILPGKVQVW   86

Qy       59  PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYE-KDAFKREHLAEVTLSVKADFP  117
             ||| ::| |||||||||||||||  || ||| || |||  |  ||||||  |||| ||||
```

```
Db       87  PEYKNRTITDMDNPRIVILALRLSDSGTYTCVIQKPDLKGAYKLEHLTSVRLMIRADFP  146

Qy      118  TPSISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSK  177
             :| |:||||||||||||||||||||||||||||||||||||  :||:||:  :||||
Db      147  VPTINDLGNPSPNIRRLICSTSGGFPRPHLWLENGEELNATNTTLSQDPETKLYMISSE  206

Qy      178  LDFNMTTNHSFMCLIKYGHLRVNQTFNWNTTK  209
             :||||| ||||| |||||  :|::| :||  :
Db      207  LDFNMTSNHSFICLVKYGDLTVSQTFYWQESK  238


RESULT 14
Q9N0T0
ID   Q9N0T0       PRELIMINARY;       PRT;   235 AA.
AC   Q9N0T0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   T-cell co-stimulatory protein B7-1.
GN   B7-1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Khatlani T., Ma Z., Onishi T.;
RT   "Cloning and Sequencing of canine cDNA encoding T-cell co stimulatory
RT   molecule B7-1.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF257653; AAF69006.1; -.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE      235 AA;  26933 MW;  C0EA51DA9FB224E3 CRC64;

Query Match             61.4%;  Score 705;  DB 6;  Length 235;
Best Local Similarity   61.5%;  Pred. No. 1.3e-55;
Matches  128;  Conservative  33;  Mismatches  47;  Indels   0;  Gaps   0;

Qy        2  LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY   61
                :|||||:||:|||||||||||||||  : :| :||||||  :|:||  :| | |||||
Db       28  LFYFCSGIIQVNKTVKEVAVLSCDYNISTTELMKVRIYWQKDDEVVLAVTSGQTKVWSKY   87

Qy       62  KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI  121
             ::| |||||||||||||||||||:|||||| ::| :|| : :|:: ||||::||||
Db       88  ENRTFADFTNNLSIVIMALRLSDNGKYTCIVQKTEKRSYKVKHMTSVMLLVRADFPVPSI  147

Qy      122  SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN  181
                ||||||||||||||||||||:||||||||||||: |||||||  :|||:| |::
Db      148  TDLGNPSHDIKRIMCSTSGGFPKPHLSWWENEEELNAANTTVSQDPDTELYTISSELDFN  207

Qy      182  MTTNHSFMCLIKYGHLRVNQTFNWNTTK  209
             :|:|||:|||||||||||  :||:||:|
Db      208  ITSNHSFVCLVKYGDLTVSQIFNWQKCK  235


RESULT 15
Q9TQS8
ID   Q9TQS8       PRELIMINARY;       PRT;   235 AA.
AC   Q9TQS8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Secreted B7-1 protein precursor.
GN   CD80.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
```

```
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20093996; PubMed=10630300;
RA   Yang S., Sim G.-K.;
RT   "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
RT   Molecules.";
RL   Immunogenetics 50:349-353(1999).
DR   EMBL; AF106825; AAF17296.1; -.
DR   EMBL; AF106831; AAF17294.1; -.
DR   EMBL; AF106829; AAF17294.1; JOINED.
DR   EMBL; AF106830; AAF17294.1; JOINED.
DR   HSSP; P33681; 1DR9.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Signal.
FT   SIGNAL        1     33       POTENTIAL.
FT   CHAIN        34    235       SECRETED B7-1 PROTEIN.
SQ   SEQUENCE   235 AA;  26917 MW;  CC08CAA676BCB40A CRC64;

Query Match             61.4%;  Score 705; DB 6;  Length 235;
Best Local Similarity   61.5%;  Pred. No. 1.3e-55;
Matches  128; Conservative   33; Mismatches   47; Indels    0;  Gaps     0;

Qy        2 LSHFCSGVIHVTKEVKEVATLSCCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY   61
            |:||||:|||||||||||| |||  ||:|:| || ||||||:::||:|| :|  ::| :|
Db       28 LFYFCSGIIQVNKTVKEVAVLSCDYNISTTELMKVRIYWQKDDEVLAVTSGQTKVWSKY    87

Qy       62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI  121
            :||| |||||||||||:| | |||||||||||  |:: | :| ||:|||||||||||:|
Db       88 ENRTFADFTNNLSIVIMALRLSDNGKYTCIVQKTEKRSYKVKHMTSVMLLVRADFPVPSI  147

Qy      122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN  181
            :|  |: :||:|||:|||||||||||||||||:|||||  ||||||||| ||:| :||||
Db      148 TDLGNPSHDIKRIMCSTSGGFPKPHLSWWENEEELNAANTTVSQDPDTELYTISSELDFN  207

Qy      182 MTTNHSFMCLIKYGHLRVNQTFNWNTTK  209
            ::||||||||:|:|||| | ||| ||||
Db      208 ITSNHSFVCLVKYGDLTVSQIFNWQKCK  235
```

Search completed: November 25, 2003, 16:46:12
Job time : 36 secs

THIS PAGE BLANK (USPTO)

OM protein - protein search, using sw model

```
                    GenCore version 5.1.6
           Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:    November 25, 2003, 16:46:16 ; Search time 30 Seconds
                                         (without alignments)
                                         1327.992 Million cell updates/sec

Title:         US-09-666-267B-8
Perfect score: 1149
Sequence:      1 GLSHFCSGVIHVTKEVKEVA........LRVNQTFNWNTTKQEHFPDN 216

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters:      673684

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Published Applications AA:*
       1:  /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
       2:  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
       3:  /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
       4:  /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
       5:  /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
       6:  /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
       7:  /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
       8:  /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
       9:  /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
      10:  /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
      11:  /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
      12:  /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
      13:  /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
      14:  /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
      15:  /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
      16:  /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
      17:  /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
      18:  /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1149	100.0	226	10	US-09-915-789A-21	Sequence 21, Appl
2	1149	100.0	288	8	US-08-592-711-2	Sequence 2, Appli
3	1149	100.0	288	9	US-09-772-102-14	Sequence 14, Appl
4	1149	100.0	288	9	US-09-837-867A-19	Sequence 19, Appli
5	1149	100.0	288	10	US-09-896-738-10	Sequence 10, Appli
6	1149	100.0	288	10	US-09-915-789A-15	Sequence 15, Appl
7	1149	100.0	288	10	US-09-962-969-19	Sequence 19, Appl
8	1149	100.0	288	11	US-09-350-202-2	Sequence 2, Appli
9	1149	100.0	288	11	US-10-032-214-278	Sequence 278, Appl
10	1149	100.0	288	12	US-10-126-088-2	Sequence 2, Appli
11	1149	100.0	288	12	US-10-041-319-7	Sequence 7, Appli
12	1149	100.0	288	15	US-10-261-101-2	GENERAL INFORMA
13	1149	100.0	473	15	US-09-910-059-131	Sequence 131, App
14	1143	99.5	492	10	US-09-845-899A-3	Sequence 3, Appli
16	1129	98.3	288	12	US-10-032-214-94	Sequence 94, Appl
17	1121	97.6	288	12	US-10-032-214-69	Sequence 69, Appl
18	1121	97.6	288	12	US-10-032-214-82	Sequence 82, Appl
19	1119	97.4	288	12	US-10-032-214-71	Sequence 71, Appl
20	1119	97.4	288	12	US-10-032-214-77	Sequence 77, Appl
21	1119	97.4	288	12	US-10-032-214-225	Sequence 225, Appl
22	1118	97.3	288	12	US-10-032-214-84	Sequence 84, Appl
23	1116	97.1	288	12	US-10-032-214-76	Sequence 76, Appl
24	1116	97.1	288	12	US-10-032-214-86	Sequence 86, Appl
25	1116	97.1	288	12	US-10-032-214-87	Sequence 87, Appl
26	1116	97.1	288	12	US-10-032-214-286	Sequence 286, App
27	1114	97.0	288	12	US-10-032-214-226	Sequence 226, App
28	1114	97.0	288	12	US-10-032-214-251	Sequence 251, App
29	1113	96.9	288	12	US-10-032-214-90	Sequence 90, Appl
30	1113	96.9	288	12	US-10-032-214-228	Sequence 228, App
31	1113	96.9	288	12	US-10-032-214-250	Sequence 250, App
32	1112	96.8	288	12	US-10-032-214-78	Sequence 78, Appl
33	1112	96.8	288	12	US-10-032-214-248	Sequence 248, App
34	1111	96.7	288	12	US-10-032-214-238	Sequence 238, App
35	1110	96.6	288	12	US-10-032-214-236	Sequence 236, App
36	1109	96.5	288	12	US-10-032-214-88	Sequence 88, Appl
37	1109	96.5	288	12	US-10-032-214-89	Sequence 89, Appl
38	1109	96.5	288	12	US-10-032-214-92	Sequence 92, Appl
39	1109	96.5	288	12	US-10-032-214-249	Sequence 249, App
40	1108	96.4	287	12	US-10-032-214-243	Sequence 243, App
41	1105	96.2	288	12	US-10-032-214-81	Sequence 81, Appl
42	1104	96.1	287	12	US-10-032-214-74	Sequence 74, Appl
43	1104	96.1	300	12	US-10-032-214-232	Sequence 232, App
44	1103	96.0	288	12	US-10-032-214-91	Sequence 91, Appl
45	1103	96.0	288	12	US-10-032-214-229	Sequence 229, App

ALIGNMENTS

```
RESULT 1
US-09-915-789A-21
;  Sequence 21, Application US/09915789A
;  Patent No. US20020168762A1
;  GENERAL INFORMATION:
;   APPLICANT: Chen, Lieping
;   TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
;   TITLE OF INVENTION:  MOLECULES
;   FILE REFERENCE: 07039-219001
;   CURRENT APPLICATION NUMBER: US/09/915,789A
;   CURRENT FILING DATE: 2002-06-04
;   PRIOR APPLICATION NUMBER: US 60/220,991
;   PRIOR FILING DATE: 2000-07-27
;   NUMBER OF SEQ ID NOS: 23
;   SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 21
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-915-789A-21

Query Match             100.0%;  Score 1149;  DB 10;  Length 226;
Best Local Similarity   100.0%;  Pred. No. 2.4e-102;
Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 70

Qy         61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 130

Qy        121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 190

Qy        181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
```

Db   191 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 226

RESULT 2
US-08-592-711-2
; Sequence 2, Application US/08592711
; Publication No. US20020115214A1
; GENERAL INFORMATION:
;   APPLICANT: June, Carl H.
;   APPLICANT: Thompson, Craig B.
;   APPLICANT: Nabel, Gary J.
;   APPLICANT: Gray, Gary S.
;   APPLICANT: Rennert, Paul D.
;   TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: LAHIVE & COCKFIELD
;   STREET: 60 State Street
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02109
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/592,711
;   FILING DATE: 26-JAN-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/435,816
;   FILING DATE: 4-MAY-1995
;   APPLICATION NUMBER: US 08/403,253
;   FILING DATE: 10-MARCH-1995
;   APPLICATION NUMBER: US 08/253,964
;   FILING DATE: 3-JUNE-1994
;   APPLICATION NUMBER: US 08/073,223
;   FILING DATE: 4-JUNE-1993
;   APPLICATION NUMBER: US 08/200,947
;   FILING DATE: 23-FEB-1994
;   APPLICATION NUMBER: US 07/864,805
;   FILING DATE: 7-APR-1992
;   APPLICATION NUMBER: US 08/247,505
;   FILING DATE: 23-MAY-1994
;   APPLICATION NUMBER: US 07/864,866
;   FILING DATE: 7-APR-1992
;   APPLICATION NUMBER: US 08/218,155
;   FILING DATE: 25-MAR-1994
;   APPLICATION NUMBER: US 07/864,807
;   FILING DATE: 7-APR-1992
;   APPLICATION NUMBER: US 07/902,467
;   FILING DATE: 16-JUNE-1992
;   APPLICATION NUMBER: US 07/275,433
;   FILING DATE: 23-NOV-1988
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Mandragouras, Amy E.
;   REGISTRATION NUMBER: 36,207
;   REFERENCE/DOCKET NUMBER: RPI-002CP4
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 227-7400
;   TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 288 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   DESCRIPTION: B cell activation antigen; natural ligand
;   DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
;   FEATURE:
;   NAME/KEY: signal sequence
;   LOCATION: -34 to -1
;   IDENTIFICATION METHOD: amino terminal sequencing of
;   OTHER INFORMATION: hydrophobic soluble protein
;   FEATURE:
;   NAME/KEY: extracellular domain
;   LOCATION: 1 to 208
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   FEATURE:
;   NAME/KEY: transmembrane domain
;   LOCATION: 209 to 235
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   FEATURE:
;   NAME/KEY: intracellular domain
;   LOCATION: 236 to 254
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   FEATURE:
;   NAME/KEY: N-linked glycosylation
;   LOCATION: 19 to 21
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   FEATURE:
;   NAME/KEY: N-linked glycosylation
;   LOCATION: 55 to 57
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   FEATURE:
;   NAME/KEY: N-linked glycosylation
;   LOCATION: 64 to 66
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   FEATURE:
;   NAME/KEY: N-linked glycosylation
;   LOCATION: 152 to 154
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   FEATURE:
;   NAME/KEY: N-linked glycosylation
;   LOCATION: 173 to 175
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   FEATURE:
;   NAME/KEY: N-linked glycosylation
;   LOCATION: 177 to 179
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   FEATURE:
;   NAME/KEY: N-linked glycosylation
;   LOCATION: 192 to 194
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   FEATURE:
;   NAME/KEY: N-linked glycosylation
;   LOCATION: 198 to 200
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   FEATURE:
;   NAME/KEY: Ig V-set domain
;   LOCATION: 1 to 104
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   FEATURE:
;   NAME/KEY: Ig C-set domain
;   LOCATION: 105 to 202
;   IDENTIFICATION METHOD: similarity with known
;   IDENTIFICATION METHOD: sequence
;   PUBLICATION INFORMATION:
;   AUTHORS: FREEMAN, GORDON J.
;   AUTHORS: FREEDMAN, ARNOLD S.
;   AUTHORS: SEGIL, JEFFREY M.

```
; AUTHORS: LEE, GRACE
; AUTHORS: WHITMAN, JAMES F.
; AUTHORS: NADLER, LEE M.
; TITLE: B7, A New Member Of The Ig Superfamily With
; TITLE: Unique Expression On Activated And Neoplastic B Cells
; JOURNAL: The Journal of Immunology
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-592-711-2

Query Match             100.0%;  Score 1149;  DB 8;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 3.3e-102;
Matches  216;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
          ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 3
US-09-772-102-14
; Sequence 14, Application US/09772102
; Patent No. US20020006413A1
; GENERAL INFORMATION:
; APPLICANT: Sobol, Robert, E.
; APPLICANT: Shawler, Daniel L.
; APPLICANT: Bartholomew, Richard M.
; APPLICANT: Carlo, Dennis J.
; APPLICANT: Gold, Daniel P.
; TITLE OF INVENTION: Genetically Engineered Tumor Cell
; TITLE OF INVENTION: Vaccines
; FILE REFERENCE: P-SD 4581
; CURRENT APPLICATION NUMBER: US/09/772,102
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,498
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/185,335
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-772-102-14

Query Match             100.0%;  Score 1149;  DB 9;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 3.3e-102;
Matches  216;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146
```

```
Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
          ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 4
US-09-837-867A-19
; Sequence 19, Application US/09837867A
; Patent No. US20020098542A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. US2002009854241e1 Forms of T Cell Costimulatory
; TITLE OF INVENTION: Molecules and Uses Therefor
; FILE REFERENCE: BWI-120CPADV
; CURRENT APPLICATION NUMBER: US/09/837,867A
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 08/205,697
; PRIOR FILING DATE: 1994-03-02
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-837-867A-19

Query Match             100.0%;  Score 1149;  DB 9;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 3.3e-102;
Matches  216;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
          ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 5
US-09-910-174A-5
; Sequence 5, Application US/09910174A
; Patent No. US20020106730A1
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. US20020106730A1e1 Members of the B7
; TITLE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174A
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 288
```

```
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-910-174A-5

Query Match             100.0%;  Score 1149;  DB 10;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 3.3e-102;
Matches  216;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy      1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     27  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  86

Qy     61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy    121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy    181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
           ||||||||||||||||||||||||||||||||||||
Db    207  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 6
US-09-896-738-10
; Sequence 10, Application US/09896738
; Patent No. US20020165347A1
; GENERAL INFORMATION:
;  APPLICANT: Fox, Michael
;  APPLICANT: Sullivan, John K.
;  APPLICANT: Fang, Mei
;  TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
;  FILE REFERENCE: 00-513-A
;  CURRENT APPLICATION NUMBER: US/09/896,738
;  CURRENT FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: 60/215,645
;  PRIOR FILING DATE: 2000-06-30
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 10
;  LENGTH: 288
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-896-738-10

Query Match             100.0%;  Score 1149;  DB 10;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 3.3e-102;
Matches  216;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy      1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     27  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  86

Qy     61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy    121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy    181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
           ||||||||||||||||||||||||||||||||||||
Db    207  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 7
US-09-915-789A-15
; Sequence 15, Application US/09915789A
; Patent No. US2002016762A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Chen, Lieping
;  TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
;  TITLE OF INVENTION: MOLECULES
;  FILE REFERENCE: 07039-219001
;  CURRENT APPLICATION NUMBER: US/09/915,789A
;  CURRENT FILING DATE: 2002-06-04
;  PRIOR APPLICATION NUMBER: US 60/220,991
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 15
;  LENGTH: 288
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-915-789A-15

Query Match             100.0%;  Score 1149;  DB 10;  Length 288;
Best Local Similarity   100.0%;  Pred. No. 3.3e-102;
Matches  216;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy      1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     27  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  86

Qy     61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy    121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy    181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
           ||||||||||||||||||||||||||||||||||||
Db    207  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 8
US-09-962-969-19
; Sequence 19, Application US/09962969
; Publication No. US20030045703A1
; GENERAL INFORMATION:
;  APPLICANT: Sharpe, Sharpe
;            Borriello, Francescopaolo
;            Freeman, Gordon
;            Nadler, Lee
;  TITLE OF INVENTION: No. US20030045703A1el Forms of T Cell Costimulatory
;                      Molecules and Uses Therefor
;  NUMBER OF SEQUENCES: 65
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: LAHIVE & COCKFIELD
;   STREET: 28 State Street
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02109-1875
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: ASCII Text
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/962,969
;   FILING DATE: 24-Sep-2001
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/702,525
;   FILING DATE: <Unknown>
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Mandragouras, Amy E.
;   REGISTRATION NUMBER: 36,207
;   REFERENCE/DOCKET NUMBER: BWI-120CPUS
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617)227-7400
```

```
        TELEFAX: (617)227-5941
  INFORMATION FOR SEQ ID NO: 19:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 288 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
      MOLECULE TYPE: protein
      SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-962-969-19

Query Match          100.0%;    Score 1149; DB 11;   Length 288;
Best Local Similarity  100.0%;   Pred. No. 3.3e-102;
Matches 216;  Conservative   0;  Mismatches   0;  Indels   0;   Gaps    0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
          ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242


RESULT 9
US-09-350-202-2
; Sequence 2, Application US/09350202
; Publication No. US2003009643A1
; GENERAL INFORMATION:
    APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
    APPLICANT: Gray, Gary S., Rennert, Paul D.
    TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
    NUMBER OF SEQUENCES: 14
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: LAHIVE & COCKFIELD
      STREET: 28 State Street
      CITY:  Boston
      STATE: Massachusetts
      COUNTRY: USA
      ZIP: 02109
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0,  Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/350,202
      FILING DATE:
      CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  08/403,253
      FILING DATE: March 10, 1995
      APPLICATION NUMBER: US 08/253,964
      FILING DATE: 3 JUNE 1994
      APPLICATION NUMBER: US 08/073,223
      FILING DATE: 4 JUNE 1993
      APPLICATION NUMBER: US 08/200,947
      FILING DATE: 23 FEB 1994
      APPLICATION NUMBER: US 07/864,805
      FILING DATE: 7 APR 1992
      APPLICATION NUMBER: US 08/247,505
      FILING DATE: 23 MAY 1994
      APPLICATION NUMBER: US 07/864,866
      FILING DATE: 7 APR 1992
      APPLICATION NUMBER: US 08/218,155
      FILING DATE: 25 MAR 1994
```

```
    APPLICATION NUMBER:  US 07/864,807
    FILING DATE: 7 APR 1992
    APPLICATION NUMBER: US 07/902,467
    FILING DATE: 16 JUNE 1992
    APPLICATION NUMBER: US 07/275,433
    FILING DATE: 23 NOV 1988
  ATTORNEY/AGENT INFORMATION:
    NAME: Mandragouras, Amy E.
    REGISTRATION NUMBER: 36,207
    REFERENCE/DOCKET NUMBER: RPI-002CP2
  TELECOMMUNICATION INFORMATION:
    TELEPHONE:  (617) 227-7400
    TELEFAX:  (617) 742-4214
  INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 288 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
      DESCRIPTION: B cell activation antigen; natural ligand
      DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
    FEATURE:
      NAME/KEY:  signal sequence
      LOCATION: -34 to -1
      IDENTIFICATION METHOD:  amino terminal sequencing of
      IDENTIFICATION METHOD:  soluble protein
      OTHER INFORMATION: hydrophobic
    FEATURE:
      NAME/KEY:  extracellular domain
      LOCATION: 1 to 208
      IDENTIFICATION METHOD:  similarity with known
      IDENTIFICATION METHOD:  sequence
    FEATURE:
      NAME/KEY:  transmembrane domain
      LOCATION: 209 to 235
      IDENTIFICATION METHOD:  similarity with known
      IDENTIFICATION METHOD:  sequence
    FEATURE:
      NAME/KEY:  intracellular domain
      LOCATION: 236 to 254
      IDENTIFICATION METHOD:  similarity with known
      IDENTIFICATION METHOD:  sequence
    FEATURE:
      NAME/KEY:  N-linked glycosylation
      LOCATION: 19 to 21
      IDENTIFICATION METHOD:  similarity with known
      IDENTIFICATION METHOD:  sequence
    FEATURE:
      NAME/KEY:  N-linked glycosylation
      LOCATION: 55 to 57
      IDENTIFICATION METHOD:  similarity with known
      IDENTIFICATION METHOD:  sequence
    FEATURE:
      NAME/KEY:  N-linked glycosylation
      LOCATION: 64 to 66
      IDENTIFICATION METHOD:  similarity with known
      IDENTIFICATION METHOD:  sequence
    FEATURE:
      NAME/KEY:  N-linked glycosylation
      LOCATION: 152 to 154
      IDENTIFICATION METHOD:  similarity with known
      IDENTIFICATION METHOD:  sequence
    FEATURE:
      NAME/KEY:  N-linked glycosylation
      LOCATION: 173 to 175
      IDENTIFICATION METHOD:  similarity with known
      IDENTIFICATION METHOD:  sequence
    FEATURE:
      NAME/KEY:  N-linked glycosylation
      LOCATION: 177 to 179
      IDENTIFICATION METHOD:  similarity with known
      IDENTIFICATION METHOD:  sequence
    FEATURE:
```

```
   ;   FEATURE:
   ;      NAME/KEY: N-linked glycosylation
   ;      LOCATION: 192 to 194
   ;      IDENTIFICATION METHOD: similarity with known
   ;         sequence
   ;   FEATURE:
   ;      NAME/KEY: N-linked glycosylation
   ;      LOCATION: 198 to 200
   ;      IDENTIFICATION METHOD: similarity with known
   ;         sequence
   ;   FEATURE:
   ;      NAME/KEY: Ig V-set domain
   ;      LOCATION: 1 to 104
   ;      IDENTIFICATION METHOD: similarity with known
   ;         sequence
   ;   FEATURE:
   ;      NAME/KEY: Ig C-set domain
   ;      LOCATION: 105 to 202
   ;      IDENTIFICATION METHOD: similarity with known
   ;         sequence
   ;   PUBLICATION INFORMATION:
   ;      AUTHORS: FREEMAN, GORDON J.
   ;      AUTHORS: FREEDMAN, ARNOLD S.
   ;      AUTHORS: SEGIL, JEFFREY M.
   ;      AUTHORS: LEE, GRACE
   ;      AUTHORS: WHITMAN, JAMES F.
   ;      AUTHORS: NADLER, LEE M.
   ;      TITLE: B7, A New Member Of The Ig Superfamily With
   ;         Unique Expression On Activated And Neoplastic B Cells
   ;      JOURNAL: The Journal of Immunology
   ;      VOLUME: 143
   ;      ISSUE: 8
   ;      PAGES: 2714-2722
   ;      DATE: 15-OCT-1989
   ;   RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-09-350-202-2

  Query Match          100.0%;  Score 1149;  DB 11;  Length 288;
  Best Local Similarity 100.0%;  Pred. No. 3.3e-102;
  Matches 216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  86

Qy   61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS  146

Qy  121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF  206

Qy  181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  216
         ||||||||||||||||||||||||||||||||||||
Db  207  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  242

RESULT 10
US-10-032-214-278
; Sequence 278, Application US/10032214
; Publication No. US20030138881A1
;   GENERAL INFORMATION:
   ;      APPLICANT: PUNNONEN, JUHA
   ;      APPLICANT: LAZETIC, ALEXANDRA
   ;      APPLICANT: LEONG, STEVEN R.
   ;      APPLICANT: CHANG, CHIA-CHUN
   ;      APPLICANT: APT, DORIS
   ;      APPLICANT: GUSTAFSSON, CLAES
   ;   TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
   ;   FILE REFERENCE: 02-1067301US
   ,  CURRENT APPLICATION NUMBER: US/10/032,214
   ,  CURRENT FILING DATE: 2002-12-20
   ;   PRIOR APPLICATION NUMBER: 09/888,324
```

```
   ;      PRIOR FILING DATE: 2001-06-22
   ;      PRIOR APPLICATION NUMBER: PCT/US01/19973
   ;      PRIOR FILING DATE: 2001-06-22
   ;      PRIOR APPLICATION NUMBER: 60/213,946
   ;      PRIOR FILING DATE: 2000-06-23
   ;      PRIOR APPLICATION NUMBER: 60/241,245
   ;      PRIOR FILING DATE: 2000-10-17
   ;   NUMBER OF SEQ ID NOS: 320
   ;   SOFTWARE: PatentIn Ver. 2.1
   ;   SEQ ID NO 278
   ;      LENGTH: 288
   ;      TYPE: PRT
   ;      ORGANISM: Homo sapiens
US-10-032-214-278

  Query Match          100.0%;  Score 1149;  DB 12;  Length 288;
  Best Local Similarity 100.0%;  Pred. No. 3.3e-102;
  Matches 216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27  GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE  86

Qy   61  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87  YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS  146

Qy  121  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF  206

Qy  181  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  216
         ||||||||||||||||||||||||||||||||||||
Db  207  NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN  242

RESULT 11
US-10-126-088-2
; Sequence 2, Application US/10126088
; Publication No. US20030170821A1
;   GENERAL INFORMATION:
   ;      APPLICANT: FREEMAN, GORDON J.
   ;               FREEDMAN, ARNOLD S.
   ;               NADLER, LEE M.
   ;      TITLE OF INVENTION: DNA Encoding B7, A New Member
   ;         Of The IgG Superfamily With Unique Expression On
   ;         Activated And Neoplastic B Cells.
   ;      NUMBER OF SEQUENCES: 4
   ;      CORRESPONDENCE ADDRESS:
   ;         ADDRESSEE: The Dana-Farber Cancer Institute
   ;         STREET: 44 Binney Street
   ;         CITY: Boston
   ;         STATE: Massachusetts
   ;         COUNTRY: U.S.A.
   ;         ZIP: 02115
   ;      COMPUTER READABLE FORM:
   ;         MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
   ;         COMPUTER: IBM Personal System 2; Model 30
   ;         OPERATING SYSTEM: MS/DOS
   ;         SOFTWARE: WordPerfect 5.0
   ;      CURRENT APPLICATION DATA:
   ;         APPLICATION NUMBER: US/10/126,088
   ;         FILING DATE: 19-Apr-2002
   ;         CLASSIFICATION: <Unknown>
   ;      PRIOR APPLICATION DATA:
   ;         APPLICATION NUMBER: US 07/751,306
   ;         FILING DATE: 28-AUG-1991
   ;         APPLICATION NUMBER: US 07/591,300
   ;         FILING DATE: 01-OCT-1990
   ;      ATTORNEY/AGENT INFORMATION:
   ;         NAME: HART, JULIA D.
   ;         REGISTRATION NUMBER: 33132
   ;         REFERENCE/DOCKET NUMBER: DFCI-116.1
```

```
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (203) 255-8900
;         TELEFAX: (203) 259-2846
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 288 amino acids
;         TYPE: amino acid
;         MOLECULE TYPE: protein
;         TOPOLOGY: linear
;       DESCRIPTION: B cell activation antigen; natural ligand
;       FEATURE:
;         NAME/KEY: signal sequence
;         LOCATION: -34 to -1
;         IDENTIFICATION METHOD: amino terminal sequencing of
;           soluble protein
;         OTHER INFORMATION: hydrophobic
;         sequence
;       FEATURE:
;         NAME/KEY: extracellular domain
;         LOCATION: 1 to 208
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       FEATURE:
;         NAME/KEY: transmembrane domain
;         LOCATION: 209 to 235
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       FEATURE:
;         NAME/KEY: intracellular domain
;         LOCATION: 236 to 254
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       FEATURE:
;         NAME/KEY: N-linked glycosylation
;         LOCATION: 19 to 21
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       FEATURE:
;         NAME/KEY: N-linked glycosylation
;         LOCATION: 55 to 57
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       FEATURE:
;         NAME/KEY: N-linked glycosylation
;         LOCATION: 64 to 66
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       FEATURE:
;         NAME/KEY: N-linked glycosylation
;         LOCATION: 152 to 154
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       FEATURE:
;         NAME/KEY: N-linked glycosylation
;         LOCATION: 173 to 175
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       FEATURE:
;         NAME/KEY: N-linked glycosylation
;         LOCATION: 177 to 179
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       FEATURE:
;         NAME/KEY: N-linked glycosylation
;         LOCATION: 192 to 194
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       FEATURE:
;         NAME/KEY: N-linked glycosylation
;         LOCATION: 198 to 200
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       FEATURE:
;         NAME/KEY: Ig V-set domain
;         LOCATION: 1 to 104
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       FEATURE:
;         NAME/KEY: Ig C-set domain
;         LOCATION: 105 to 202
;         IDENTIFICATION METHOD: similarity with known
;         sequence
;       PUBLICATION INFORMATION:
;         AUTHORS: FREEMAN, GORDON J., FREEDMAN, ARNOLD S.
;           SEGIL, JEFFREY M., LEE, GRACE, WHITMAN, JAMES F.
;           NADLER, LEE M.
;         TITLE: B7, A New Member Of The Ig Superfamily With
;           Unique Expression On Activated And Neoplastic B Cells
;         JOURNAL: The Journal of Immunology
;         VOLUME: 143
;         ISSUE: 8
;         PAGES: 2714-2722
;         DATE: 15-OCT-1989
;       RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
;     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-126-088-2

  Query Match          100.0%;  Score 1149;  DB 12;  Length 288;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-102;
  Matches 216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242


RESULT 12
US-10-041-319-7
; Sequence 7, Application US/10041319
; Publication No. US2003018309A1
; GENERAL INFORMATION:
;   APPLICANT: Immunex Corporation
;   APPLICANT: Baum, Peter R.
;   APPLICANT: DuBose, Robert F.
;   APPLICANT: Wiley, Steven R.
;   TITLE OF INVENTION: HUMAN B7 POLYPEPTIDES
;   FILE REFERENCE: 3176-A
;   CURRENT APPLICATION NUMBER: US/10/041,319
;   CURRENT FILING DATE: 2002-01-07
;   NUMBER OF SEQ ID NOS: 17
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 288
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-041-319-7

  Query Match          100.0%;  Score 1149;  DB 12;  Length 288;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-102;
  Matches 216;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
```

```
Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
```

RESULT 13
US-10-261-101-2
; GENERAL INFORMATION:
; APPLICANT: Ostrand-Rosenberg, Suzanne
;   Baskar, Sivasubramanian
;   Glimcher, Laurie H.
;   Freeman, Gordon J.
;   Nadler, Lee M.
; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/261,101
; FILING DATE: 30-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,148
; FILING DATE: 27-Sep-2000
; APPLICATION NUMBER: 08/147,772
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; JOURNAL: The Journal of Immunology
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-10-261-101-2
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match   100.0%; Score 1149; DB 15; Length 288;
Best Local Similarity   100.0%; Pred. No. 3.3e-102;
  Matches 216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
```

Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

RESULT 14
US-09-910-059-131
; Sequence 131, Application US/0910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: full-length human B7.1-murine ASB7 Fd fusion
US-09-910-059-131

Query Match   100.0%; Score 1149; DB 10; Length 473;
Best Local Similarity   100.0%; Pred. No. 6.4e-102;
  Matches 216; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
         ||||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
```

RESULT 15
US-09-845-899A-3
; Sequence 3, Application US/09845899A
; Patent No. US20020147326A1
; GENERAL INFORMATION:
; APPLICANT: CHAIKIN, MARGERY ANN
; APPLICANT: LYN, SALLY DOREEN PATRICIA
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: P50496
; CURRENT APPLICATION NUMBER: US/09/845,899A

```
;   CURRENT FILING DATE: 2001-04-30
;   PRIOR APPLICATION NUMBER: 09/202,346
;   PRIOR FILING DATE: 1999-01-13
;   PRIOR APPLICATION NUMBER: US 60/043,948
;   PRIOR FILING DATE: 1997-02-19
;   PRIOR APPLICATION NUMBER: US 60/038,915
;   PRIOR FILING DATE: 1997-02-21
;   NUMBER OF SEQ ID NOS: 27
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 492
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-845-899A-3

Query Match             99.5%;   Score 1143;  DB 10;  Length 492;
Best Local Similarity  100.0%;   Pred. No. 2.6e-101;
Matches  215;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy    1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

Qy   61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146

Qy  121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206

Qy  181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPD 215
          |||||||||||||||||||||||||||||||||||
Db  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPD 241

Search completed: November 25, 2003, 16:51:48
Job time : 31 secs
```

THIS PAGE BLANK (USPTO)